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Description	O43353 homo sapien	O9dz10 mus musculu	09zsd8 lycopersico	09zsd9 lycopersico		ᄰ	O9stu7 arabidopsis						082754 arabidopsis	O9v2v6 homo sapien	Oglva9 arabidopsis	O9m8c2 arabidopsis	023719 arabidopsis	O9v3q6 drosophila	Q39886 glycine max
· ID	043353	090ZT0	Q9ZSD8	60SZ60	024027	Q9Y572	Q9STU7	Q9M8C1	Q9S7D5	09м8С3	065833	Q9SFN9	082754	Q9Y2V6	60VJ60	Q9M8C2	023719	90EA60	039886
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11.2	11.1	11.1	11.0	11.0	11.6	10.9	10.5	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.6	10.6	10.6	10.6	10.5	10.5	10.5	10.5	
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ALIGNMENTS

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۵	43353	PRELIMINARY:	PRT:	540 AA.	
Ų					
Ę	1998		06, Created)	_	
턴	-		Last	sequence update)	date)
E	_		Last	annotation update)	update)
Ю	SERINE/THREONINE KINASE		<i>:</i>		•
z	RICK OR RIP2.				
Š	Homo sapiens (Human)	(Human).			
ပ္	Eukaryota; Metazoa;			ata; Vert	Craniata; Vertebrata; Euteleostomi;
ပ္	Mammalia; Eutheria;	heria; Primates;		rhini; Hc	Catarrhini; Hominidae; Homo.
×	NCBI_TaxID=9606;	906;			
z	[1]				
ب۵	SEQUENCE FROM N.A.	1 N.A.			
×	MEDLINE=9824]	MEDLINE=98241596; PubMed=9575181;	9575181;		
Ą	Inohara N., c	lel Peso L.,	Koseki T.,	Chen S.,	Nunez G.;
Ħ	"RICK, a nove	al protein ki	nase conta	ining a c	"RICK, a novel protein kinase containing a caspase recruitment domain,
E	interacts with	h CLARP and	regulates	CD95-medi	ated apoptosis.";
J.	J. Biol. Chem	1. 273:12296-	12300(1998		J. Biol. Chem. 273:12296-12300(1998).
Z,	[3]				
بم	SEQUENCE FROM N.A.	1 N.A.			
4	Ozersky P., P	Ozersky P., Holmes A., Broy M.;	λ M.;		
ij	Submitted (J)	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases	e EMBL/Ge	nBank/DDE	J databases.
z	[3]				
<u>a</u> ,	SEQUENCE FROM	I N.A.			
×	MEDLINE-98307	MEDLINE-98307936; PubMed-9642260;	3642260;		
Ą	McCarthy J.V., Ni	, Ni J., Dixit V.M.;	Lt V.M.;		
E	"RIP2 is a nc	vel NF-kappal	3-activati	ng and ce	"RIP2 is a novel NF-kappaB-activating and cell death-inducing
E+	kinase.";				
4	J. Biol. Chem	J. Biol. Chem. 273:16968-16975(1998).	16975(1998		
z	[4]				
بە	SEQUENCE FROM N.A.	I N.A.			
K	Thome M., Hot	mann K., Bur	IS K., Mar	tinon F.,	Thome M., Hofmann K., Burns K., Martinon F., Bodmer JL.,
Ą	Mattmann C., Tschopp J.;	Tschopp J.;			
E	"Identificati	on of CARDIA	(, a RIP-1	ike kinas	"Identification of CARDIAK, a RIP-like kinase that associates with
E	caspase-1.";		•		
д:	Curr. Biol. 8:0-0(1998).	1:0-0(1998).			
Z 1	[5]				
, ب۵	SEQUENCE FROM N.A.	N.A.			
ď۰	Platzer M., \	Platzer M., Varon R.; S.hmittod (NBC-1000) to the man //confort detables	Tuna C	400	1000 C
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Kinase

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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ETHYLENE TRIDUCIBLE CTRI-LIKE PROTEIN KINASE.
Lycopersicon esculentum (Tomato).
Eukaryopta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solaname.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                            SAVPLVSREELKKLEFVGKGGFGVVFRAHHRTWNHDVAVKIVN-----SKKISWEV 62
                                                                                                                                                                                                                                                                                                                                SALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREA 67
Pazdernik N.J., Donner D.B., Goebl M.G., Harrington M.A.;
"Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting
a Death Domain but Induces Apoptosis and Activates NF-kappaB.";
Mol. Cell. Biol. 19:0-0(1999).
EMBL; AFI78953; ARR93133.1; -.
INTERPRO; IPR000119; -.
INTERPRO; IPR001245; -.
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28.0%; Pred. No. 2.6e....
24.ve. 70; Mismatches 192;
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PRINTS: PR0109; TYRKINASE.

PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                            540;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                            575A692239505792 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          Score 2823; DB 4;
Pred. No. 1.9e-220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                               PFAM; PF00069; pkinase; 1.
PFAM; PF00619; CARD; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR INTERACTING PROTEIN 3.
                                                                                                                                                                                                                              61194 MW;
    AAC24561.1; -AAC27722.1; -AAC25668.1; -AAC25668.1; -AAC25668.1; -AAD04634.1; -
                                                                                                                                                                                                                                                                            99.8%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                   HSSP; P00523; 2PTK.
INTERPRO; IPR000719; -.
INTERPRO; IPR001315; -.
INTERPRO; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wus musculus (Mouse)
                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 539; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                    AF064824;
AF117829;
                                        AF078530;
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                      AC004003
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461

090ZL0 090ZL0;

RESULT 090ZL0

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PS00107; PROTEIN_KINASE_ATP; 1. PS00108; PROTEIN_KINASE_ST; 1. PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang Y., Li N.;
Plant Physiol. 114:1135-1135(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (Tomato)
                                                                                                                        Best Local Similarity 34.0 Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 SFSTIMDMLRPHLKS 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 SFLKCLIELEPVLRT
                                                          829 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                             Kinase.
SEQUENCE
               PROSITE;
PROSITE;
                                                                                                          Query Match
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Eukaryota; Viridiplantue; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                        HR--KTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSRFKANTFLSSKTAAGTPE-----WMAPEVIRDEPSNE-----KSDVKSFGVILWELA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                     GEAICSALPT------IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERP
                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                           DB 10; Length 806;
                      "Ethylene-inducible tomato CTR1-like protein kinase.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AFI10519; AAD10057.1; -.
RHSZP: P06213; ITRK.
RIWTERPRO; IPR000719; -.
RIWTERPRO; IPR001245; -.
RHTERPRO; IPR001240; -.
RHTERPRO; IPR001240; -.
RPAM; PF00069; pkinase; 1.
RPRIWTS; PR00109; TYRINASE.
RPROSITE; PS00110; PROTEIN_KINASE_ATP; 1.
RPROSITE; PS00110; PROTEIN_KINASE_ATP; 1.
RPROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. AILSA CRAIG;
Kannan P., Giovannoni J.J.;
"Ethylene-inductible tomato CTR1-like protein kinase.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF110518; AAD10056.1; -.
                                                                                                                                                                                                                               806 AA; 89387 MW; 9102529F49549A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ETHYLENE INDUCIBLE CTR1-LIKE PROTEIN KINASE.
                                                                                                                                                                                                                                                                        Query Match 13.8%; Score 389.5; DB 10; Best Local Similarity 34.0%; Pred. No. 4.5e-23; Matches 107; Conservative 55; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    829 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P06213; 1IRK.
INTERPRO; IPR000719; -.
INTERPRO; IPR001245; -.
INTERPRO; IPR002290; -.
PFAM; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || : | |: SFSTIMDMLRPHLKS 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4081;
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                  Kinase
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SEGUENCE FROM N.A.

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ZEGEOUTH H., Jones B., Frasse P., Marty C., Maitre B., Latche A.,

Rech J.C., Bouzayen M.;

Pech J.C., Bouzayen M.;

Tethylene-regulated gene expression in tomato fruit: characterization of novel ethylene-responsive and ripening-related genes isolated by differential display.";

In Plant J. 18:589-600(1999).

REMBL; Y13273: CAA7372.1; -

REMBL; AF095250; AAD46406.1; -

REMBL; AF095250; AAD46406.1; -

REMPL; PRO00719; -

REPRAM; PRO0059; PKINASE_ATP; 1.

REPRAM; PRO017E; PROUBENLKINASE_ATP; 1.

REPRAM; PRO1169; PROTEIN_KINASE_ATP; 1.

REPROSITE; PS00110; PROTEIN_KINASE_DM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eŭkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HR--KTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSKWRMMSLSQSRSSKSAPFGGTIIYMPPE--NYEPFGQKSRASIKHDIYSYAVITWEVL 223
                                                                                                                                                                                                                                                                                                                                                            --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERP 281
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                             3 GEAICSALPT-----IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                     EQDFHAERL----KEFLREVAIMKRLRHPNIVLFWGAVIQPPNLSIVTEYLSRGSLYRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: | || : || || : || || || 642 HKPGAKKVLDERRPL--CLAYDVANGMNYLHKRNPPIVHRDLKSPNLLVDKKYTVKICDF
                                                                                                                                                                    49;
                                                                                                 Length 829;
                                                                                                                                                                    Indels
91889 MW; 9E976BF7640CE11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 91.9 KDA PROTEIN.
                                                                                             13.8%; Score 389.5; DB 10; 34.0%; Pred. No. 4.6e-23; ive 55; Mismatches 104;
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Gaps
HKARESYIFPILGICNEPEF ----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRIL 125
                                                                        HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185
                                                                                            186 EGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQ 244
                                                                                                                                                                                                                         245 GHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEIT 301
                                                                                                                                                                                                                                            20 DLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLRE----AEILHKA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY'2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TREMBLRel. 15, Last annotation update)
122A6.310 OR AT4G24480.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Buaryota; Adicoryledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
                     65 ASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFWENGSLSGLLQSQCPRP---WPLLCRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Zimmentann W., Wambutt R., Kalicki J., Wohldmann Zimmenmann W., Grueneisen A., Wambutt R.F.X.; Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 359.5; DB 10; Length 963; 31.7%; Pred. No. 1.5e-20; Live 60; Mismatches 105; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft
Bevan H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALOY8637; CAB45083.1; --
EMBL; ALO18561; CAB79358.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107993 MW; 10DD8910F44C140E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 963 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PF00069; pkinase; 1.
PRONTOS; TYRKINASE.
PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
Hypothetical protein.
SEQUENCE 963 AA; 107993 MW; 10DB8910F
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                 302 FLEAVIQLKKTKLQSVSSA 320
                                                                                                                                                                                                                                                                                                                                   293 NMNAAVSTVKDFLSQLKSS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR000719; -. INTERPRO; IPR001245; -. INTERPRO; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
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Matches 9
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                                                                                                                   12;
                                                                                                                                                                                SKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSR 225
                                                                                                                                                                                                                                                                                                                                                                                                   283
                                                                                                                                                                                                                                                                  641
                                                                                                                                                                                                                                                                                                     HRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGL 167
                                                                                                                                                                                                                               50 --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEAICSALPT------IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-99272740; Pubmed-10339433;
Yu P.W., Huang B.C., Shen M., Quast J., Chan E., Xu X., Nolan G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Payan D.G., Luo Y.; "Identification of RIP3, a RIP-like kinase that activates apoptosis
                                                                                                                                                                                                                                                  226 KOPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                   45;
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                                                                              Length
                                                                          13.6%; Score 385.5; DB 10; Length 33.2%; Pred. No. 9.8e-23; ive 56; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 AA; 56901 MW; 38A3ECFBEBBD4151 CRC64;
                       08FCF7468993537D CRC64;
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Last annotation update)
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       Hypothetical protein; Kinase.
SEQUENCE 829 AA; 91912 MW;
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EMBL; AF156884; AAD39005.1;
HSSP; PO8631; 1AD5.
INTERPRO; IPRO00719; -.
INTERPRO; IPRO01245; -.
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2000 (TrEMBLrel. 15,
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                                                                                                                   Matches 104; Conservative
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803 STIMDMLRPHLKS 815
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                                                                                               Similarity
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                                 PRELIMINARY;
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INTERPRO; IPR000719; -.
INTERPRO; IPR001245; -.
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Best Local Similarity
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EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 PILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYE 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F5E6 genomic sequence.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC020580; AAF63631.1; -.
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brasslcaceae; Arabidopsis.
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                                                                                   RFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKT - - EYPDVAWPLRFRI - - - - - LH
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                                                                                                                                                                                                                                                                                                                                                                                                                                             244 QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PROTEIN KINASE, PUTATIVE.
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Pred. No. 3.8e-20;
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32.0%;
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Best Local Similarity 32.09
Matches 94; Conservative
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SEQUENCE
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Q9M8C1 Q9M8C1;

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RESULT

09M8C1

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RESULT

13; 61 VAVKIMDPSTTSAVTKAHKKTFQKEVLLLSKMKHDNIVKFVGACIEPQLI-1VTELVEG 119 215 176 KLADFGIAR-----EETRGGMTC-EAGTSKWMAPEVYSPEPLRVGEKKEYDHKADIYSF 228 275 Gaps 44 VAVKHLHHT--PLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101 276 NPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNI 335 ---IGTTL 312 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacee; Arabidopsis. 102 SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEF-HV 216 AVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQ 161 KIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEP-----GQKSRASIKHDIYSY 59: Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F., Length Bloecker H., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier Salanoubat M.; Indels EU Arabidopsis sequencing project; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL13299; CABG4442.1; -. EMBL; AL049862; CAB42902.1; -. EU Arabidopsis sequencing project; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases 370 AA; 42328 MW; A508F716B432804B CRC64; 03S7D5; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) PROTEIN KINASE ATNI-LIKE PROTEIN. T3A5.110 OR F18B3.10. Arabidopsis thaliana (Mouse-ear cress). --RMSSDSS--DB 10; 63; Mismatches 106; ch 12.3%; Score 348.5; DB 1 1 Similarity 29.2%; Pred. No. 3.2e-20; 94; Conservative 63; Mismatches 106 PFAM; PF00069; PKinase; 1.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

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AILSA CRAIG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassicales; Bra
NCBI_TaxID=3702;
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01-OCT-2000
                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 PGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEE-SLPYD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 IPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVS 318
                                                                                                                                                                                                                                                                                                                                                       24 LSRGASGTVSSARHADW-RVQVAVKHL---HIHTPLLDSERKDVLREAEILHKARFSYIF 79
                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassloaliophyta; eudicoryledons; core eudicots; Rosidae; eurosids II;
Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                           TRAIN—CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Maitl R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thallana chromosome III BAC F5E6 genomic sequence.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                       505 LFMGAVTLPQGLCIVSEFLPRGSLFRLLQRNMSKLD--WRRRINMALDIARGMNYLHRCS
                                                                                                                                                                                                                                                                                                                                                                                                                           PPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYE
                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 348.5; DB 10; Length 763; llarity 31.9%; Pred. No. 8.7e-20; Conservative 57; Mismatches 109; Indels 45;
                                                                                                                                                                                                                                                                  763 AA; 85593 MW; F6787110603C597C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                              Last sequence update)
Last annotation update)
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                               763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07,
07,
15,
                                                  01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                             EMBL; AC020580; AAF63629.1;
                                                                                  PROTEIN KINAŠE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 SAIHLCDKKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LSDKNK 721
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTR2 PROTEIN.
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O65833;
O1-AUG-1998 (
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01-OCT-2000
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SEQUENCE
                                          09MBC3;
                               09M8C3
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            RESULT
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67 AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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STRAIN-CV. COLCHBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome I BAC F25P22 genomic sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC012679; AAF24836.1;
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        804 DVAXGMDCLHTSNPTIVHRDLKSPNLLVDTDWNVKVCDFGLSRLKHNTFLSSKSTAGTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE-----RKDVLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKOPFEDVTNPLQIMYSVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 QCHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     913 QNKRLEIPKELDPI-----VARIIWECWQTDPNLRPSFAQLTVALTPLQR 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%; Score 340; DB 10; Length 96
30.8%; Pred. No. 6e-19;
ive 56; Mismatches 108; Indels
Lin Z., Hackett R.M., Payton S., Grierson D.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ005077; CAA06334.1; --
HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                 04522B40F3425068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                INTERPRO; IPR002290; -.
PFAM; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00449; ATPASE_A; UNKNOWN_L.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                        MENDEL, 29910, Lyces;2342;29910.
INTERPRO; IPR000568; -.
INTERPRO; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    981 AA; 107175 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00069; pkinase; 1. PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.0°
Best Local Similarity 30.8°
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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INTERPRO; IPRO00719; -.
INTERPRO; IPR001245; -.
INTERPRO; IPR002290; -.
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11;

E47D333311805B52 CRC64;

82281 MW;

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736 AA;
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SEQUENCE 83
       SEQUENCE
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                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                 89 EFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLK 148
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Peters S.A., van Staveren M., Dirkse W., Stiekema W., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 GTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRA
                                                                                                                                                                                               Length 1030;
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Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
PRINTS; PR00308; ANTIFREEZEI.
PROSTTE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSTIE; PS00108; PROTEIN_KINASE_ST; 1.
PROSTIE; PS50011; PROTEIN_KINASE_DOM; 1.
Hypothetical protein.
SEQUENCE 1030 AA; 112205 MW; 9BD7125FBIDF1B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031018; CAA19821.1; -.
EMBL; AL161558; CAB79260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                               Query Match 11.9%; Score 337.5; DB 10; Best Local Similarity 34.8%; Pred. No. 1e-18; Matches 93; Conservative 39; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00989; PAS; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-OCT-2000 (TrEMBLrel. 15, Last and
PUTATIVE SERINE/THREONINE KINASE.
F7H19.240 OR AT4G23050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 MISLIESGWAQNPDERPSFLKCLIELE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                  65 REAEILHKARFSYIFPILG-ICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPL--- 120
                                                                                                                                                                                                                121 -RFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSR 179
                                                                                                                                                                                                                                                              624
                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                            238 IMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 REAEILHKARFSYIFPILGIC-NEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 APEGGIIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 SALPTIPYHKLADLRY---LSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQ
                                                                                                                                                                                                                                                                                                                                          | | |: :| || || :- || || || SGKGTPQ-----WCDVFSFGVILWELMTTLVPW-DRLNSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei Y.J., Ding J.F., Xiong H., Zhou Y., Hui R.T., Liew C.C.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF116826; AAD29632.1; -.
                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) HYPOTHETICAL 92.9 KDA PROTEIN.
Score 335.5; DB 10;
Pred. No. 9.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.8%; Score 334.5; DB 4; Best Local Similarity 28.1%; Pred. No. 1.3e-18; Matches 116; Conservative 76; Mismatches 170;
                 11.9%; Score 335.5;
ilarity 32.9%; Pred. No. 9.3e
Conservative 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR00019; .
INTERPRO; IPR001145; .
INTERPRO; IPR002110; .
INTERPRO; IPR002110; ..
PFAM; PF00069; pkinase; 1.
PRINTS; PR00109; TYRINIASE.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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835 AA;
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               Query Match
Best Local Similarity
Matches 79; Conserv
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TISSUE-HEART;
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18;
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                                                                     624 -- OPGNLRWMAPEVFT -- OCTRYTIKADVFSYALCLWEILTGEIPFAHL-KPAAAAADMA 678
                                            244 QGH-RPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITF 302
                                                                                                                               LEAVIQLKKTKLQSVSSAIHLCDKK------KMELSLNIPVNHGPQEESCG- 347
                                                                                                                                                                62 DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYP-DVAWPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RFRILHEIALGVNYLHNMTPPLLHHDLKTQNILL-DNEFHVKIADFGLSKWRMMSLSQSR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 KGFWIFEAGIYRWAAPELFSYDILEIGEKKHYDHKVDVYSFAIVFWELLINKIPFKGKNN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 SSKSAPEGGTIIYMPPENY----EPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 PLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 -IFVAYAASKNORPSV--ENLPEGV-----VSILOSCWAENPDARPEFKEITYSLTNLL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTFEEITFLEAVIQLKKTKL---QSVSSAIH---LCD------KKKMELSLNIP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: | :| | :| | :| | 335 RSLSSDT--DATSSNSKANIATEDSTSSLVQERVVCDCPGLKMSKTRKLKKKTNKLMNMI 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 TIPYHKLADLRYLSRG---ASGTVSSARHADWR--VQVAVKHLHIHTP----LLDSERK 61
                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PROTEIN KINASE ATHALLIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Bukasryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
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                                                                                                                                                                                                                       348 -SSQLHENSGSPETSRSLP-APQDN-DFLSRKAQDCYFMKLHHCPGNHSWDST 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match Best Local Similarity 30.1%; Pred. No. 7.1e-19; Matches 112; Conservative 64; Mismatches 135; Indels 61;
                                                                                                                                                                                                                                                        405 AA; 46012 MW; C7C4CF29E8DA3111 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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DNA Res. 7:31-63(2000).
EMBL; AB018119; BAA97277.1; -.
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Search completed: June 14, 2001, 08:06:41 Job time: 132 sec

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Eucalyptus grandis
                                                        Skin cell protein,
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                                                                                                         Murine RIP
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W04627
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B50439
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Y45047
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971L-0121199.
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05-JUN-1997;
30-JUN-1997;
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     Human B1 protein.
Amino acid sequenc
Human cancer assoc
Human RICK protein
Human RICK protein
Human RICK protein
Human RICK protein
Busast and ovarian
                                                                                                                                                                    June 14, 2001, 08:04:28; Search time 51.9 Seconds (without alignments) 594.762 Million cell updates/sec
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**Sidesdydgata/geneseq/gene
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Listing first 45 summaries

    protein search, using sw model

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New B1 protein regulates cell death and cell survival pathways derivatives, DNA and antibodies, also regulate intracellular

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Wallach

Boldin M, Malinin N, WPI; 1999-070258/06

N-PSDB; X02558.

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Baughn MR; .
H, Azimzai Y;
         /note= "protein kinase family signature sequence"
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tone GA, Yue
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Bandman O, Au-Young J,
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Shih LL;
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N-PSDB; Z46143.
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Patterson C, Bandm
Reddy R, Lu DAM,
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12-JAN-1999;
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                                            This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
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                                                                                                                                                                                          Length 540;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                         100.0%; Score 2829; DB 20;
100.0%; Pred. No. 5.2e-257;
Live 0; Mismatches 0;
  cancer
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 inflammation; for treating AIDS,
                        Claim 4; Fig 3A; 90pp; English.
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ID Y68774 standard; Protein; 540
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Matches 540;
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                                                                   v68769-95 and Y68797-99 represent. human phosphorylation effectors (PHSP), designated PHSP1-PHSP1 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from CDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, the diagnosis, treatment and prevention of proliferative disorders, pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antigonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMY 240
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antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                    KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPL 120
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                prevention of proliferative, immune and neuronal disorders
 human phosphorylation effectors useful for the diagnosis,
                                                                                                                                                                                                                                                                                    Length 540;
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Pred. No. 1.9e-
0; Mismatches
                                                                                                                                                                                                          with increased PHSP expression/activity.
                                            Page 84-85; 142pp; English.
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Matches 539;
                                            Claim 1;
                                                                                                                                                                                                                                     Sequence
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C77607 to C78448 encode the human cancer associated proteins given in B4339 to B44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cycostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiathmatic; antitinflammatory: antidabetic; antitinflammatory: antidabetic; antitinflammatory: contiting; antiallergic; antibacterial; antiviral; dermatological; antitingroid; antibacterial; antiviral; dermatological; corresponded; antipaoriatic and antiangiogenic. The polymotleotides and polympetides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymotleotides, antibodies, aponists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the present
               dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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Pred. No. 1.9e-256;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating or diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1595-1597; 2352pp; English.
                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
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99.8%;
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Best Local Similarity 99.8
Matches 539; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; C77779
                                                                                                                                           Homo sapiens.
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caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; rNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autolimnune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; parkinson; s disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-4S; CARD-4Y;
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                                                         SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
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98US-0099041.
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301..43
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17-JUN-1998
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Domain
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Novel CARD-3 and CARD-4 genes and polypeptides used or treating

WPI; 1999-494269/41. N-PSDB; 209246.

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This invention describes the isolation of moves in a proteins and a partial murine CARD-12 and CARD-4 polynocleotides and proteins of partial murine CARD-14 protein and genes. The genes and proteins of partial murine CARD-14 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation.

The caspase recruitment domain (CARD) polynocleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and probpylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of complex, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the Ras/APO-1 receptor complex, abnormal activity of the rank may be treated include cancer complex, abnormal activity of a caspase. Diseases that may be treated include cancer complex, and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosis, immune-mediated glomerulonephritis), viral in p53 and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosis, immune-mediated glomerulonephritis), viral infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spindal muscular dystrophy, cerebellar celegeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4F gene can express a long transcript that encodes CARD-4F, and CARD-4Z. This sequence control of the human CARD-4 spince variants, cardial in the method of the
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regulation of cellular proliferation and differentiation and cell
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                                                                                                  novel human
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Pred. No. 6.9e-256;
0; Mismatches 2;
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                                                            2; 181pp; English
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illarity 99.6%;
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Matches 538; Conserv
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LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEI

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This sequence is the human RICK (RIP-like interacting CLARP kinase)
protein of the invention. The RICK protein acts as a positive regulator
of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10
during CD95 signalling. The invention provides methods for identifying
apoptosis signalling pathway inhibitors and activators, and methods and
compositions for screening compounds which will modulate the interactions
of the various compositions identified: ACK, RICK, and the CIDE family of
activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening
confositions for agents, useful in the diagnosis, prognosis or treatment of
disease associated with excess cell growth and dysregulation of
confositions complexes containing RICK and CLARP can be used in drug
screening assays to identify inhibitor molecules blocking CD95-mediated
confositions of the enzymantic activity of caspase-8.

Confosition of ARC-like inhibitory compounds may be useful for gene
therapy treatment of disease with increased cell death in muscole tissue
confosition of ARC-like inhibitory compounds may be useful for gene
therapy treatment of disease with increased cell death in muscole tissue
confosition of ARC-like inhibitory compounds may be useful for gene
therapy treatment of disease with increased cell death in muscole tissue
can deadiac disorders. Therapeutic compositions of CIDEs can be used
as reagents for the preparation or affinity chromatography
media, and for diagnostically measuring RICK levels: A specific inhibitor
confortion with intracellular factors such as CLARP and FADD appears to
confortion with intracellular factors such as CLARP and FADD appears
confortion with intracellular discorders.

Confortion with intracellular discorders are poptential drug candidates.
                                                                                                                                                                                                                                                                                       RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; C1095 signalling; apoptosis signalling pathway; C10E-A; C10E-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
  481 ptrtskvrqlldttdiggeefakvivgklkdnkqmglqpypeilvvsrspslnllgnksm 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koseki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 7a; 93pp; English.
                                                                                                             Y59404 standard; Protein; 531
                                                                                                                                                                                                                                                  Human RICK protein sequence.
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N-PSDB; 248762.
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                                                                   RESULT
Y59404
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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
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                                                                                                        310 KKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQD
                                                                                                                                                                                                      430 RLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQ
                                             LGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGT
                                                                                           190 IIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPV
LHKARFSYIFFILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIA
                                                                                                                                          250 INEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQL
                                                                                                                                                                                                                                                                                                                                    490 LLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                 Human RICK protein sequence residues 54-531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koseki T;
                                                                                                                                                                                                                                                                                                                                                                                                                   Y59405 standard; Protein; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inohara N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nunez G,
                                                                                                                                                                                                                                                                                                                                                                                                                                         X59405;
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Score 2774; DB 21; Length 531; Pred. No. 7.4e-252; ; Mismatches 1; Indels 0;

1;

98.18; 99.68;

Best Local Similarity 99.6 Matches 529; Conservative

Similarity

Query Match

us-09-445-223-1.rag

RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; cIDE-8; DREP-1; Atlanoais; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.

Human RICK protein sequence residues 248-531.

21-MAR-2000 (first entry)

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Kinase) protein of the invention. RICK acts as a positive regulator

Kinase) protein of the invention. RICK acts as a positive regulator

Cof apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

during CD95 signalling. The invention provides methods for identifying

apoptosis signalling pathway inhibitors and activators, and methods and

compositions for screening compositions and activators, and methods and

compositions for screening compositions identified: RCK, RICK, and the CIDE family of

activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

cof the various compositions identified: RCK, RICK, and the CIDE family of

activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

cof assays for agents, useful in the diagnosis, prognosis or treatment of

disease associated with excess cell growth and dysregulation of

apoptosis. Complexes containing RICK and CLARP can be used in drug

screening assays to identify inhibitor molecules blocking CD95-mediated

apoptosis. Overexpression of ARC in an in vitro cell system can be used

confortification of ARC-11ke inhibitory compounds may be useful for gene

charapy treatment of disease with increased cell death in muscle tissue

confortification of ARC-11ke inhibitory compositions of CIDEs can be used to

charapy treatment of disease with increased cell death in muscle tissue

conformation with intracellular factors such as CLARP and FADD appears to

cof an essential step in the blochemistry of apoptosis is needed. RICK

interaction with intracellular factors such as CLARP and FADD appears to

be essential factors are potential drug candidates.

Confortions are potential drug candidates.

Confortions are potential drug candidates.

Confortions in the preparation of RICK binding to intracellular apoptosis factors are potential drug candidates.
Claim 6; Page -; 93pp; English.
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0; Gaps Length 478; Indels Score 2497; DB 21; pred. No. 6.7e-226; 0; Mismatches 1; 88.3%; 99.8%; Query Match 88.3' Best Local Similarity 99.8' Matches 477; Conservative

; 0

Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases

Claim 6; Page -; 93pp; English.

Koseki T;

(UNMI) UNIV MICHIGAN Nunez G, Inohara N, WPI; 2000-072163/06.

99WO-US09183. 98US-0069023,

27-APR-1999; 27-APR-1998;

04-NOV-1999.

Homo sapiens W09955134-A2

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63 VLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRF 122
                                               123 RILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSK 182
                                                            242
                                                                                                          422
                                                                                                                                                                                                                                                                       301 slpapgdndflsrkagdcyfmklhhcpgnhswdstisgsgraafcdhkttpcssalinpl 360
                                                                                                                                                                                                                                                                                                 STAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPT 482
                                                                                                                                                                                                                                                                                                            09
            SAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV
                                                                                                                                              SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITF
                                                                                                                                                           LEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSR
                                                                                                                                                                                                                                               SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPL
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Length 284;
                          Indels
Query Match 52.1%; Score 1475; DB 21; Best Local Similarity 100.0%; Pred. No. 3.1e-130; Matches 284; Conservative 0; Mismatches 0;
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483 RTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540

421

ò g Y59406 ID Y59406 standard; Protein; 284 AA.

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Gaps

This sequence is a fragment of the human RICK (RIP-like interacting CLARP Kinase) protein of the invention. RICK acts as a positive regulator of apoptosis; potentiating apoptosis; induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compositions identified: RICK, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening compositions for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug compositions of apoptosis overexpression of ARC in an in vitro cell system can be used apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

Conditional of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to therapy treatment of disease with increased cell death in muscle tissue can be used as reagents for the preparation or affinity chromatography can be used as reagents for the preparation or affinity chromatography can be used as reagents for the preparation or affinity chromatography can be used in the intracellular factors such as CLARP and FADD appears to apprecial parents in the blochemistry of apoptosis is needed. RICK and the preparation or affinity chromatography apprecase that for apoptosis of RICK binding to intracellular. apoptosis factors are potential drug candidates. Note: This sequence was created using information given in the 284 AA; specification Sednence

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This sequence is a fragment of the human RICK (RIP-like interacting CLARP Kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentialing and caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ACK, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREF-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Owexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

C identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntirRICK antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICK; human, RIP-11ke interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemla; ischaemic injury; toxin-induced liver disease.
                                                                                                                                                   436
                                     QQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDI 496
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                                                                                                                                               AQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIA
317 VSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                               QGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human RICK protein sequence residues 365-531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y59407 standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US09183
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can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.

Note: This sequence was created using information given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thytoiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative collitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular
                                                                                                                                                                                                                                                     374 SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433
                                                                                                                                                                                                                                                                                                                   493
                                                                                                                                                                                                                                                                                                                                  Breast and ovarian cancer associated antigen protein sequence SEQ ID
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                     434 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT
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                                                                                                                                                                                          Length 167;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                            Page 1086; 1299pp; English
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                                                                                                                                                                                                         Best Local Similarity 100.
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-611515/58.
                                                                                                                                            167 AA;
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                                                                                                            specification.
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                                                                                                                                              Seguence
                                                                                                                                                                                        Query Match
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(IMMV) IMMUNEX CORP.

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breast and ovarian cancer. Included in the invention are sequences breast and ovarian cancer. Included in the invention are sequences ($72032 - $72040 and $859129 which are used in the isolation are sequences characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; breast and ovarian cancer. The nucleic acid sequences, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune chircipal and ulcerative colitis; cardiovascular disorders such as mycoardial ischaemias; wound healing; neurological diseases such as erebral anoxia and epilepsy; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a death associated kinase with ankyrin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 YMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Death associated kinase protein containing ankyrin repeats; DAKAR;
kinase; quality assurance agent; shelf life; marker.
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/note= "this region contains a series of nine
tandem ankyrin repeats"
                                                                                                                                                                                                                                                                                                                                               Length 153;
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7.297
5.ee "N-terminal kinase domain"
                                                                                                                                                                                                                                                                                                                                              Score 797; DB 21;
Pred. No. 5.9e-67;
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                                                                                                                                                                                                                                                                                                                                                            Pred. No. 5.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 VITWEVLSRKOPFEDVTNPLQIMYSVSQGH 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               28.2%;
99.3%;
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98US-0099973.
99US-0119353.
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Matches 149; Conservative
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                                                                                                                                                                                                                                                                     Infectious diseases.
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Misc-difference 1
                                                                                                                                                                                                                                                                                                  153
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11-SEP-1998;
09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1999;
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                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                 Query Match
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The present sequence represents a murine death associated kinase protein, containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides can be used to express the polypeptides, and as probes to identify mucleic acids encoding proteins having kinase activity. DAKAR polypeptides are used for purifying proteins, e.g. to measure protein activity, as quality assurance agents to monitor shelf life and stability of binding partner proteins; as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds which may interfere with a poptosis; as molecular weight and isoelectric focusing markers; as controls for peptide fragmentation; identification of unknown proteins, e.g. by comparison with proteins in databases; and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography. The antibodies can also be used to block binding of the protein, and to purify the protein by immunoaffinity or enhance the kinase activity of DAKAR can be used to treat diseases characterized by overproduction or upregulated production of DAKAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
                                                                                                                                      Novel death associated kinase containing ankyrin repeats (DAKAR) used as molecular weight marker and as controls for peptide fragmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 PLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNGEA----ICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 IELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----tfqeit-----setedlcekpdeevk---dlahepgekssl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 -----HHCPGNHSWDSTIS--GSQRAAF-----CDHKTTPCSSAIINPLSTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pssssgkrlsgvssvdsafssrgslslsfereastgdlgptd1gkklvdaii----sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 megegrgrwalgllrtfdagefagwekvgsggfgqvykvrhvhwktwlaikcspslhvd-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 PDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSQSRSSKSAPEG--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVTNPLQIMYSVSQGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSQLHENSGSPETSRSLPAPQDNDF-------LSRKAQDCYFMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Mismatches 160; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 577; DB 21;
Pred. No. 3.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 NSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDA 462
                                                                                                                                                                                                  Claim 13; Page 10; 71pp; English.
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 172; Conservative
                                                                            WPI; 2000-195582/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 AA;
                                      Virca
                                                                                                    N-PSDB; Z61161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                      Bird TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348
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67 AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH
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                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                                   239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences V75942-Y76123 represent polypeptides encoded by cDNA sequences V75942-Y76121 represent polypeptides encoded by cDNA sequences V75942-Y76121 represent polypeptides and hair cell ypes. Sequences V75942-Y76121, Y76020-Y76021, Y76019 and Y76104-Y76102 are proteins with one or more putative transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murison JG;
                                                                                                                                                                                                                                                                                                                                                        Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides useful for the treatment of various conditions including wounds and cancer {\ }^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kumble A,
                                                                                                                                                                                                                                                                                                                Murine protein kinase/ankyrin homologue, SEQ ID NO:334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onrust R,
:: || :: |: |: | :: | 420 dtsrl----mkilgpgdvdlvldssas1lhlavea 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 195-196; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sleeman M, Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                     Y76079 standard; Protein; 787
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                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Z61784.
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                                                                                                                                                                                                                                                            27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09955865-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                        Y76079;
                                                                                                    RESULT 11
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Murison JG;
                                                                 244 QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
                                                                                                                                                                                                                                                                                                                                                                                                    301 TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET 360
                                                                                                                                                                                                                                                                                                                                                322 krasappfdndcslsellsqldsgisqtlegpeelsrsssec---klpssssgkrlsgvs 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases .
                                              127 EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE
                                                                                                                G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS
                                                                                                                                   t------setedlcekpdeevk---dlahepgeksslesksearpessrl
                                                                                                                                                                                                                                                                                                                 SRSLPAPQDNDF-----HHCPGNH
                                                                                                                                                                                                                                                                                                                                                                                 SWDSTIS--GSQRAAF-----CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; noctropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumble KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 262-263; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skin cell protein, SEQ ID NO: 334
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429 lqpqdvdlvldssasllhlavea 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B56018 standard; Protein; 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 IQSKREDIVNQMTEACLNQSLDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-007495/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1999;
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10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66

Pred. No. 4.6e-45; 64; Mismatches 154; Indels 116;

Length 787;

DB 21;

20.4%; Score 576; 33.6%; Pred. No. 4.

Conservative Similarity

Matches 169;

Query Match Local

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20;
keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukcoytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skin; dermal papilla; keratinocyte; neonatai foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; andyogenesis; tumour vaccularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                               G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRSLPAPQDNDF-----HCPGNH 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 krasappfdndcslsellsgldsgisgtlegpeelsrsssec---klpssssgkrlsgvs 378
                                                                                                                                                                                                                                                                                                                                                       AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH 126
                                                                                                                                                                                                                                                                                                                                                                              EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGHRPVINEESLPYDIPHR -- - ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      svásafssrgslslsfereastgálgptálgkklváaii----sgátsrl----mki 428
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                     10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66
                                                                                                                                                                                                                                                                                                                  lrtfdagefagwekvgsggfgqvykvrhvhwktwlaikcspslhvd----drermellee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 kghrp----elppicrprpracasliglmgrcwhadpgvrp-----tfqei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t------setedlcekpdeevk---dlahepgeksslesksearpessrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWDSTIS--GSQRAAF-----CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW
                                                                                                                                                                                                                                                   64; Mismatches 154; Indels 116;
                                                                                                                                                                                                                  Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory; cytostatic; neuroprotective; vulnery.
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                                                                                                                            oligonucleotides for examining expression patterns.
                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                Score 576; DB 22;
Pred. No. 4.6e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y76123 standard; Protein; 590 AA.
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429 lqpqdvdlvldssasllhlavea
                                                                                                                                                                                                                20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                              787 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2000
                                                                                                                                                                                                                                                     Matches 169;
                                                                                                                                                               Sequence
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y76123;
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Y76123
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WO9955865-A1

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The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, Keratinocyte stem cells and translat amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate anglogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences V5543-Y7613 represent polypeptides encoded by CDNA sequences derived from several mouse, rat or human skin cell types. Sequences Y7544-Y7547, Y7602-Y7601, Y76044-Y76104 and Y76119 are proteins with an N-terminal signal sequence. Indicating that they are secreted. Sequences Y7586-Y75989, Y76061-Y7601, Y76109
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                                                                                                                                                                          Murison JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
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322 krasappfdndcslsellsqldsgisqtlegpeelsrsssec---klpssssgkrlsgvs 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           akkmemakfryilpvygicqep--vglvmeymetgslekllase----plpwdlrfrivh 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66
                                                                                                                                                                                                                                                             Novel polynucleotides useful for the treatment of various conditions including wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LSRKAQDCYFMKL-----HHCPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 lrtfdagefagwekvgsggfgqvykvrhvhwktwlaikcspslhvd----drermellee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 kghrp----elppicrprpracasligimgrcwhadpgvrp-----tfgei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 590;
                                                                                                                                                                          Kumble A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Score 574; DB 21; 33.4%; Pred. No. 4.5e-45; ive 65; Mismatches 154;
                                                                                                                                                                          a,
                                                                                                                                                                            Onrust
                                                                                                                                                                                                                                                                                                                      Claim 4; Page 231-232; 235pp; English.
                                                                                                                                                                          Watson JD,
                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                    98US-0069726.
98US-0188930.
                                                  99WO-NZ00051
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                                                                                                                                                                            Sleeman
                                                                                                                                                                                                              WPI; 2000-072177/06
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Matches 168; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 AA;
                                                                                                                                                                                                                                   N-PSDB; Z61830
                                                  29-APR-1999;
                                                                                      29-APR-1998;
                                                                                                       09-NOV-1998;
                                                                                                                                                                            Strachan L,
               04-NOV-1999
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EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPF 186
                 TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET 360
                                                                                                                                                                                                                                             393 SWDSTIS--GSQRAAF------CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 439
                                                                                                                                                                                                                                                                                                       | || | || :| :| :| :| 379 svdsafssrgslslsfereastgdlgptdigkkklvdaii-----sqdtsrl-----mki 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of murine Fel, a novel protein kinase. The sequence represents translation (reading frame 3) of Genesis clone 971025TRAMO04820HT (see 258584). The invention relates to purified murine polypeptides having kinase function (see Y79152-56) and isolated nucleic acids encoding them (see Z58582-86). Claimed vectors comparising the novel nucleic acids, and claimed host cells (bacterial, yeast, plant, insect or animal) transfected or transduced with the vectors, are used to produce the polypeptides.
                                                        G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS
                                                                         --setedlcekpdeevk---dlahepgeksslesksearpessrl
                                                                                                               QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
                                                                                                                                                                                                                              -----HHCPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel murine polynucleotides encoding kinase polypeptides, used a probes to identify nucleic acids encoding proteins having kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fel; protein kinase; mouse; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marken JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Y79154 standard; Protein; 763
                                                                                                                                                                                                                                                                                                                                            440 IQSKREDIVNOMTEACLNOSLDA
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                                                                                                                                                                                                                            361 SRSLPAPQDNDF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murison JG;
----CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 439
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                  nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 574; DB 22; Length 590; ilarity 33.4%; Pred. No. 4.5e-45; Conservative 65; Mismatches 154; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kumble KD,
                                                                                                                                                                                                                                                                   Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 309-310; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                        Skin cell protein, SEQ ID NO: 409.
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                                                                                                                                                      B56062 standard; Protein; 590
                                                    440 IQSKREDIVNOMTEACLNOSLDA
                                                                       :|: |:| : |:: | 429 | Igpgdvdlvldssasllhlavea
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SWDSTIS--GSQRAAF-
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Best Local Simi
Matches 168;
                                                                                                                                                                                                            08-MAR-2001
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                                                                                                                                                                                 B56062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 QKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 SSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF---- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HHCPGNHSWDSTIS--GSQRAAF- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 lsqldsglsqtlegpeelsrsssec---klpssssgkrlsgvssvdsafssrgslslsfe 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 HHDLKTONILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG--GTIIYMPPENYEPG 201
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    27 GASGIVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLREAEILHKARFSYIFPILG 83
                                                                                                                                                                                                                                                                                                                                                                                                                         The kinase polypeptides and their fragments are used as mol.wt. and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses, as kinases play a central role in cellular signal transduction. As such, alterations in kinase expression and/or activation can have a profound effect on a plethora of cellular processes, e.g. prolipeptides could also be used to identify binding partner proteins, or as reagents to identify proteins that regulate or interact with them. They may also be used for preparation of antibodies useful for detection, purification, and for blocking binding of kinase polypeptides to their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 HR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 setedlcekpdeevk---dlahepgeksslesksearpessrlkrasappfdndcslsel
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                                                                                                                                                                                                                                                                                                                                                             Indels 116;
                                                                                                                                                                                                                                                                                                                   Query Match 20.3%; Score 574; DB 21; Length 763; Best Local Similarity 34.2%; Pred. No. 6.8e-45; Matches 166; Conservative 62; Mismatches 142; Indels 11:
                                                                                                                                                                                                                                                               763 AA;
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hlavea 427
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Search completed: June 14, 2001, 08:07:36 Job time: 188 sec

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                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                  5258287-23
US-07-946-497-1
US-08-483-322-1
US-08-478-882-1
US-08-451-4058-2
US-08-496-841C-137
                    US-09-296-715-25
US-07-920-281C-1
US-08-46-277-1
US-08-487-826B-13
US-09-247-373B-33
US-09-247-373B-33
US-08-330-108-1
US-08-32-10087-1
US-08-101-593-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FESTENG for Windows Version 2.0b
CARRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/09/019,942
              09-247-373B-25
                                                                                                                                                                                                             US-08-628-417-5
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09019942
Patent No. 6033855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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99.8%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
REGISTRATION NUMBER: 35,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1931 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.8
Matches 1868; Conservative
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CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-09-019-942-2
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4324.869 Million cell updates/sec
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Sequence 66,
Sequence 24,
Sequence 2, A
Sequence 2, A
Sequence 1, A
Sequence 10,
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Sequence 2,
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/cgnl_//ptodata/l/ina/PcTUS_COMB.seq:*
                       Compugen Ltd.
                                                                                  June 13, 2001, 15:39:37 ; Search time
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US-08-261-432-1
US-08-261-432-1
US-08-587-680A-24
US-09-329-418-2
US-09-329-418-1
US-08-545-196B-10
US-08-545-196B-12
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US-09-188-930-257
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PCT-US93-07347-1
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US-08-265-087-3
US-08-621-493-3
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          GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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2098
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Match Length DB
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Perfect score:
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Db 1092 TTTGA QY 1198 gttac	 Db 152 GTTAC Ov 1258 gaage	1212	1272	0 71 0	1392	1452 AT	1512	Db 1572 AGCC	1632	1/38 t 1692 T	1752 A	1812	UY 1910 agga Db 1872 AGGA	RESULT 2 US-08-700-575- ; Sequence 31,	GENERAL INF GENERAL INF APPLICANT APPLICANT APPLICANT	; APPLICANT ; TITLE OF ; NUMBER OF ; CORRESPON		
12 GTCAGCTCTGGTTCGGAGAAGCAGCGGCTGGCGTGGGCCATCCGGGGGAATGGGCCCTC	Oy 118 gtgacctagtgttgcggggcaaaaagggtcttgccggcctcgttgcaggggggtatc 177	Oy 178 tgggggcctgagggggggggggggggggggggggggggg	Oy 238 accggcctgagcgcccgggaccatgaacgggggccatctgcagcgccctgccaccat 297	Oy 298 tecetaccacaaactegecgacetgegetacetgageegeetetggeactgtgte 357	Oy 358 gtccgccacgcagactggcgcgtccaggtggccgtgaagcactgcacatccacac 417	Oy 418 tccgctgctcgacagtgaaagaaugttttaagagaagctgaattttacacaaagc 477	Oy 478 tagatttagttacatttttccaatttgggaatttgcaatgagcctgaattttgggaat 537 	Oy 538 agttactgaatacatgccaaatggatcattaaatgaactcctacataggaaagctgaata 597 	Oy 598 tcctgatgttgcttggccattgagatttcgcatcctgcatgaaattgcccttggtgtaaa 657	Oy 658 ttacctgcacaatatgactcctctcttacttcatcatgacttgaagactcagaatatctt 717	Oy 718 attggacaatgaatttcatgttaagattgcagattttggtttatcaaagtggcgcatgat 777 	Oy 778 gtccctctcacagtcacgaagtagcaaatctgcaccagaaggaggacaattatttat	Oy 838 gccacctgaaaactatgaacctggacaaaaatcaagggccagtatcaagcacgatatata 897 	Oy 898 tagctatgcagttatcacatgggaagtgttatccagaaaacagcctttgaagatgtcac 957 	Oy 958 caatcctttgcagataatgtatagtgtcacaaggacatcgacctgttattaatgaaga 1017 	Oy 1018 aagtttgccatatgatatacctcaccgagcacgtatgatctctctaatagaaagtggatg 1077	Oy 1078 ggcacaaaatccagatgaaagaccatcttcttaaaatgtttaatagaacttgaaccagt 1137 	Oy 1138 tttgagaacatttgaagataactttcttgaagctgttattcagctaaagaaaacaaa 1197
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ctetteageaataataeateeaeteteaaetgeaggaaaeteagaaegtetgeagee 1557
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                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
ANT: Au-Young, Janice
ANT: Handman, Olga
ANT: Hawkins, Phillip R.
ANT: Hawkins, Phillip R.
ANT: Wilde, Craig G.
OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
SPONDENCES 45
SPONDENCE ADDRESS:
RESSEE: INCYTE PHARMACEUTICALS, INC.
TO PALO ALTO
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XY: USA
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287 ctgcccaccattccctaccacaaactcgccgacctgcgctacctgagccgcgggcgctct 346
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Patent No. 5367065

GENERAL INFORMATION:
GENERAL INFORMATION:
CECHERAL OSSEPH R.
APPLICANT: Ecker, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: No. 536706511s
STREET: One Liberty Place - 46th Floor
                  Length 3516;
                                    Pred. No. 3.4e-14;
0; Mismatches 316;
                DB 4;
                   Score 102.4;
                  4.9%;
                                  Best Local Similarity 51.83
Matches 372; Conservative
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COMPUTER READABLE FORM:
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CITY: Philadelphia
STATE: PA
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                   Query Match
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Patent No. 615502

GENERAL INFORMATION:
APPLICANT: Wateson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: OF INVENTION: And APPLICANT: Marthew
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000-1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.0%; Score 210; DB 1; Best Local Similarity 100.0%; Pred. No. 4.4e-39; Matches 210; Conservative 0; Mismatches 0;
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                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: BILLINGS, LOCY J
REGISTRATION NUMBER: 36749
REFERENCE/DOCKET NUMBER: SP-100 US
TELEPHONE: 415-855-055
TELEPHONE: 415-855-055
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: THP-1 Phorbol LPS
US-08-700-575-31
                                                                                                                                                                                                                                                                                                 LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                   FILING DATE:
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LENGTH: 3516
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GENERAL INFORMATION:
   APPLICANT: Ecker, Joseph R.
   APPLICANT: Kieber, Joseph J.
   TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ADDRESSEE: Norris
STREET: One Liberty Place - 46th Floor
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              COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,464
FILING DATE: 19920810
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81.4; DB 1; Pred. No. 1.8e-09; 0; Mismatches 201;
                                                                                                                                                                     ALLONALIS MILLER, SUZABNO E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2890 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%;
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.1;
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                        LENGTH: 2890 base pai
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 118..2583
US-07-928-464-1
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                       linear
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PCT-US93-07347-1
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1988 TGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGG 2047
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APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2168 TIGACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTC 2210
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                                                                                                                                           Patentin Release #1.0, Version #1.25
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Pred. No. 1.8e-09;
0; Mismatches 201;
                                                                                                                                                               19930805
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-08-003 311B-1; Sequence 1, Application US/08003311B; Patent No. 5444166
                                                                                                                                                                                                                                                                                                             32,279
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.1%;
Matches 202; Conservative
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2890 base pairs
TYPE: nucleic acid
                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                COMPUTER READABLE FORM:
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118..2583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                       FILING DATE:
                    19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
PCT-US93-07347-1
                                                                                                                                             SOFTWARE:
COUNTRY:
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STRANDEDNESS:
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; LOCATION:
US-08-261-432-1
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                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: No. 544166ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tggacaatgaatttcatgttaagattgcagattttggtttatc 762
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Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                    COMPUTER REGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/003,311B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UPN-1108
TITLE OF INVENTION: and Mutations
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNET LOCAT X. Beardell REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
INFORMATION FOR SEC ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: January 12, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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Best Local Similarity 50.1%;
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                       NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 118..2583
US-08-003-3118-1
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                                                                                                                                                               COUNTRY: U
ZIP: 19103
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GCCACCCTAACATTGTTCTCTTCATGGGTGCGGTCACTCAACCTCCAAATTTGTCAATAG 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 ccgcccgccacgcagactggcgcgtccaggtggccgtgaagcacctgcacatccacact 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 cgctgctcgacagtgaaagaaaggatgttttaagagaagctgaaattttacacaaagcta 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 gatttagttacatttttccaattttgggaatttgcaatgagcctgaatttttgggaatag 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 ctgatgttgcttggccattgagatttcgcatcctgcatgaaattgcccttggtgtaaatt 659
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                                         GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph R.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602332zis
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LOTI Y: Beardell
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPN-1864
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Sequence 1, Application US/08261432 Patent No. 5602322
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WordPerfect 5.1
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118..2583
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944 tttgaagatgtcaccaatcctttgcagataatgtatagtgtgtcacaaggacatcgacct 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 aaacatgatgtatacagcttcgccattgtgatctggggtgtgtgcttacacagaataatcca 672
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                                                                                                                                                                                           764 aagtggcgcatgatgtccctctcacagtcacgaagtagcaaatctgcaccagaaggaggg 823
                                                                                                                                                                                                                                  824 acaattatttatatgccacctgaaaactatgaacctggacaaaaatcaagggccagtatc 883
382 gtgggcatgaacttcctgcattgcatgtctccgccactgctgcacctagacctgaagcca 441
                                                                                                                             442 gogaacatettgetggatgeceactaceaaatgteaagatttettgaetttgggetggee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SURTHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILTER NOW PRESS OF CONTROL TO THE PROPERTY OF CONTROL TO THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/567,375 FILING DATE: 04-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24. Application US/08587680A Patent No. 597434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C. APPLICANT: Wang, Gor-Llang
APPLICANT: Song, Wen-Yuang
APPLICANT: Scabo, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/POCKET NUMBER: 0
TELECOMMUNICATION INFORMATION:
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   2108 ATCTTCACAATCGCAATCCTCCAATTGTGCATAGAGATCTAAAATCTCCAAACTTATTGG 2167
                                                                                                    660 acctgcacaatatgactcctcctttacttcatgacttgaagactcagaatatcttat 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 ctgcgcaccttcgacgccggcgaattcgcaggctgggagaaggtgggctcgggcggcttc 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 cacatccacactccgctgctcgacagtgaaagaaaggatgtttaagagaagctgaaatt 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cttggtgtaaattacctgcacaatatgactcctcttacttcatcatgacttgaagact 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 tttttgggaatagttactgaatacatgccaaatggatcattaaatgaactcctacatagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09
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Pred. No. 8.1e-09;
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SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 50.6%;
Matches 365; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1690)
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                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-188-930-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-188-930-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647
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1962 ccgtgagtattaaagcttwawwraargktctttsrktaaatattagtctccctccatgac 2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1297 GIGGGIGCCGTIGAGTCTGAGATCCAAACAAAAGACTGTTAAACGGCTGGACTTCTTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 0.0021;
0; Mismatches 83;
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APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REPERENCE: PHM. 70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FRALESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 1;
Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09329418 Patent No. 6096539
                           REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
         30628
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%;
Best Local Similarity 48.1%;
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.6%;
Best Local Similarity 55.6%;
Matches 104; Conservative
                                                                                                                                                                      LENGTH: 1558 base pairs
TYPE: nucleic acid
GTRANDEDNESS: single
                                                                                                              TELEX: 200291
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1537 AAAAAAAAAAAA 1550
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         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1557
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-
                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-455-550-7
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APPLICANT: MUBAKAMI, KAZUO
APPLICANT: UENO, NAOTO
APPLICANT: KATO, YUKIO
APPLICANT: KATO, YUKIO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                          515 aatgagcctgaatttttgggaatagttactgaatacatgccaaatggatcattaaatgaa 574
                                                                                                                                                                                                                                                                                                                                       455 gaagctgaaattttacacaaagctagatttagttacatttttccaattttgggaatttgc 514
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                                                                                                                                                                                                                                                  Length 1554;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                             Score 61.8; DB 2;
Pred. No. 3.9e-05;
0; Mismatches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPENTING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NDTA:
RPPLICATION NUMBER: US/08/455,550
FILING DATE: 31-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7, Application US/08455550
; Patent No. 5670338
                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: cDNA (partial)

US-08-587-680A-24
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
                                                                                                                                                                                                                                             Query Match 2.99
Best Local Similarity 49.89
Matches 156; Conservative
                                                                                                       STRANDEDNESS: single
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ADDRESSEE: Dike, Bro
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                                                                                       nucleic acid
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COUNTRY:
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                                                                                                    398 accagaacccggtgctcctgcaccgggacctcaagccatccaacgtcctgctggacccag
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APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
2.6%; Score 54.2; DB 3; Length 1873;
Best Local Similarity 55.6%; Pred. No. 0.0022;
Matches 104; Conservative 0; Mismatches 83; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ZENECA LIMITED
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
TITLE PERENNCH: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 10, 608pplication US/08545196B
Patent No. 6080597
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo Sapiens
US-09-329-418-1
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1970 attaaagcttwawwraargktctttsrktaaatattagtctccctccatgacactgcagt 2029
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ZIF: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATIS: TREE FO-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN)
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREE: BIRCH, STEWART, KOLASCH AND BIRCH, STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53.6; DB 3;
Pred. No. 0.0029;
5; Mismatches 120;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
                                                                                                                                                                                                                                   2121-110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08545196B Patent No. 6080577 GENERAL INFORMATION:
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.68;
                                                                                                                                                                                                                                                                                                                                              LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6
Best Local Similarity 49.2
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                      CLASSIFICATION:
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US-08-545-196B-12
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ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-07-867-106-2
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                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                  Length 1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDRNCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 538955
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Score 53.6; DB 3;
Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 120;
                                                                                 NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REGISTRATION NUMBER: 3150
RELEPRONCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGHH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
               APPLICATION NUMBER: US/08/545,196B FILING DATE: 19-OCT-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
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Patent No. 5389526
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9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                  2.6%;
                                                                      ATTORNEY/AGENT INFORMATION:
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Matches 122; Conservative
CURRENT APPLICATION DATA:
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; MOLECULE TYPE:
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Pred. No. 0.006;
5; Mismatches 118; Indels 0
                                                                                                                REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                    PCT/AU90/00530
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                                                                      NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                                                                                                                                                                                                                                                                                          DNA (genomic)
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                                       FILING DATE: 02-NOV-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity 49.6'
Matches 121; Conservative
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APPLICATION NUMBER: APPLICATION NUMBER:
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em_esthum11:*
em_esthum12:*
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em_esthum15

em_esthum20: em_esthum21:

em_esthum22:*
em_esthum23:*
em_esthum24:*
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em_esthum27:*

em_estinl:* em_estin2: em_estin3: em_estin4:

em_estin5: em_estom1: em_estom2:

em_estov1: em_estov2: em_estpl1:

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(without alignments)
9530.371 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Sequence:
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em_estp16

em_estp19

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em_estpl2

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gb_est46: gb_est47:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	DB I	174	140	140	136	111	24	110	122	136	102	3	144	144	18	103	3	165	117	
	Ouery Match Length DB ID	811	870	828	989	641	592	909	647	654	615	645	839	1112	616	762	568	917	518	
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	Score	745.8	989	655.8	621.8	609.4	592	590.6	588.8	587	561	558.6	554	550.4	546.8	542	532.6	513.4	506	
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C 19 478.2 22.8 483 19 Al343247 AA315575 EST187344 AA315804 AA315818 AA315804 AA313804 AA313804 AA313805 AA833413 KCS-ST030 AA820715 KCS-ST030 AA820730 AA820730 AA820730 AA820730 AA313805 AA30.4 20.9 940 169 BF796292 AA3138094 AA374167 A1380917 KCS-ST030 AA313805 AA3138094 AA374167 A1380917 KA313804 AA374167 A138091 AA31547 AA3138094 AA374167 A138091 AA31547 AA312833 AA374167 A138091 AA31547 AA312833 AA37353 AA373308 SA316 AA3167 A13809 AA314167 A13809 AA3154 AA3167	DECITOR BELTOAGO BELT

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Best Local S:
Matches 694
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BE875947
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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TITLE
JOURNAL
COMMENT
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tal: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

CON distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM9669 row: g column: 24

High quality sequence stop: 739.

Location/Qualifiers

Location/Qualifiers
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Average insert size 1:1 kb. Library constructed by Life
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Pred. No. 2.7e-140;
0; Mismatches 15;
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/organism="Homo sapiens"
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ilarity 97.2%;
Conservative
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Best Local Simil
Matches 762; C
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AUTHORS
TITLE
JOURNAL
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/tissue_type="large_cell carcinoma, undifferentiated"
/lab_host."DH10B (phage-resistant)"
/note="Corgan: lung: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Casaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 828)

NIH-MGC http://mgc.noi.nih.gov/.

NIH-MGC http://mgc.noi.nih.gov/.

Ontact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Errausbergenih.gov
Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 795.

High quality sequence stop: 795.
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                                                                                                                              540 TACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGG 599
Gaps
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98.4%; Pred. No. 1.2e-133;
tive 0; Mismatches 7;
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/db_xref="taxon:9606"
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/clone_llb="NIH_MGC_69"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      /note="Vector: pr713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NoL_CGAP_GG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made 1160m the same library (clonens 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " subtraction by 118 c 135 g 208 t
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/lab_host="DH108"
                                                                                                                                                                                            /organism="Homo sapiens"/db_xref="taxon:9606"
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ACCESSION VERSION KEYWORDS SOURCE JOURNAL

COMMENT

TITLE

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/dev_stage="adult"
/lab_host="DH10B"
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Unpublished (1997)
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TITLE
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cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Seq primer: 40UP from Gibco

High quality sequence stop: 402.
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/ Organism="Homo sapiens"

/ Ab_xref="taxon:9606"

/ Clone="ImAGE:2629959"

/ Clone="ImAGE:2629959"

/ Clone="ImAGE:2629959"

/ Lissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"

/ lab_host="PHIOB"

/ lab_host="PHIOB"

/ lab_host="Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                            AW150819 641 bp mRNA EST 03-NOV-1999 xg39f08.x1 NCI_CGAP_Utl Homo sapiens CDNA clone IMAGE:2629959 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ;, mRNA
                                                                                                                                                                                                                                                Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 641)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.7e-123;
9; Mismatches 17; Indels
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       215 t
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                 AW150819.1 GI:6198717
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Best Local Similarity 95.9%;
Matches 613; Conservative 9
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AUTHORS
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FEATURES

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Parayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image/image/image.html
Insert Length: 673 .Std Error: 0.00

Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI745575 592 bp mRNA EST 17-DEC-1999 wc34f12.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2317103 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I to bases I to 592.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2026
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                                                                                                                                                                                                                                                                                                                        tgittcataaaaggatatittatatctctgitgctttgacttttttttatataaaatccgig 1966
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                                                   341 TTACTAGACACTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAATTG 282
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                                                                                                      ttactagacactactgacatccaaggagaagatttgccaaagttatagtacaaaattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:2317103"
/clone_lib="NCI_CGAP_Pr28"
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Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 885 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 470.
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                                                                                                                                                                                                                                                                                                                                                                                           Score 590.6; DB 110; Length 606;
Pred. No. 2.3e-119;
6; Mismatches 1; Indels 1;
                                                                                                                            /clone="IMAGE:2553606"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                           1. 606
/organism="Homo sapiens"
/db_xref="taxon:9606"
              Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.2%;
Best Local Similarity 98.7%;
Matches 598; Conservative
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this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                     taccoggaaatacttgtggtttctagatcaccatctttaaatttacttcaaaataaaagc 1876
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 654)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Compublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                          BES36247 654 bp miRNA EST 09-AUG-2000 601062632F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449311 5',
                                                                                                                                gactatgaacttgttagtaccaagcctacaaggacctcaaaagtcagacaattactagac 1735
                                                              1736 actactgacatccaaggagaagaatttgccaaagttatagtacaaaaattgaaagataac 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lnd.gillnl.gov.co.column: 08
High quality sequence stop: 650.
                                                                                  Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc.
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Pred. No. 1.4e-118;
0; Mismatches 11;
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    /organism="Homo saptens"

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/clone="IMAGE:3449311"
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97.6%;
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Matches 638; Conservative
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1 (bases 1 to 647)

Hegde, P., Gi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                     AW960501 647 bp mRNA EST 01-JUN-2000 EST372572 MAGE resequences, MAGF Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element CDNA microarray mopublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528

Fax: 301 838 0208
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 1924 tttatatctctgttgctttgacttttttttatataaaatccgtgagtattaaagcttwaww 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT 433
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                 cctggtatagcccagcagtggatccagagcaaaagggaagacattgtgaaccaaatgaca
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1. .647
/organis="Hono sapiens"
/db.xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 588.8; DB 12
Pred. No. 5.7e-119;
0; Mismatches 7;
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128 c 141 g 213 t
                                                                                                                                                                                                                                      AW960501.1 GI:8150185
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98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: johng@tigr.org
Plate: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.7
Matches 604; Conservative
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(#937233) Homo sapiens cDNA clone
                                                                                                                                                                         /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549.011"
                                                /organism="Homo sapiens"
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/clone="IMAGE:1185111"
/clone=lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
/signet ring cell features"
/lab_host="DH10B"
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Pred. No. 7.2e-113;
9; Mismatches 4;
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2q49cil.rl Stratagene hNT neuron
IMAGE:633044 5', mRNA sequence.
AA160647
quality sequence stop: 421.
Location/Qualifiers
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97.4%;
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similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ;, mRNA
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                 aagaccactccatgctcttcagcaataataaatccactctcaactgcaggaaactcagaa
                                                                                                                                                                                            AATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCT
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AUTHORS
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Cilone_Inb="NHHMGC_20"

(issue_type="melanotic melanoma"

/issue_type="melanotic melanoma"

/issue_type="melanoma"

/issue_type=
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NIH-MGC http://mgc.ncl.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW854 row: d column: 04
High quality sequence stop: 636.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF125028 839 bp mRNA EST 24-OCT-2000 601/52510F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025427 5' mRNA sequence.
BF125028
ccatgaaaatagtggttctcctgaaacttcaaggtccctgccagctcctcaagacaatga 1371
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Pred. No. 2.6e-111;
0; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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94.8%;
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Ledy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags 97044478
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                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28412 rev2 from Amersham
High quality sequence stop: 373.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.4e-112;
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 26.2%;
al Similarity 89.1%;
675; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1112)

NH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lo Oppublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM856 row: b column: 13

High quality sequence stop: 566.

Location/Qualifiers

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                                                                                                         TGGAGCCTTGGGAGCCGCCGCAGCAGGGGGCACACCCGGAACCGGCCTGAGCGCCCCGGG
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                        Indels
Score 550.4; DB 144;
Pred. No. 1.6e-110;
0; Mismatches 71; In.
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

RESULT 13

BF125423

LOCUS

source

FEATURES

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/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 762)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT067-023.html
&t3=190199&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                         1802 atgggtcttcagccttacccggaaatacttgtggtttctagatcaccatctttaaattta 1861
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399 GAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACT 340
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                                                                                     339 GACATCCAAGGAGAAGATTTGCCAAAGTTA-AGTACAAAAATTGAAAGATAACAAACAA
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Tel: (301) 496-1550
Tel: (301) 496-1550
Tel: (301) 496-1550
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llni.gov/Dbrp/Jimage/Jimage.html
Insert Length: 680 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
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                                                                                 AI307810 616 bp mRNA EST 08-APR-1999
tb28d07.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055661 3',
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/tissue_type="? pooled tumors (clear cell type)"
/lab_host="DH10B"
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26.1%; Score 546.8; DB 18
Best Local Similarity 96.4%; Pred. No. 9.4e-110;
Matches 559; Conservative 9; Mismatches 11;
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into the pUC 18 vector. Reverse-transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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                                                     25.8%; Score 542; DB 103;
ilarity 90.3%; Pred. No. 1.1e-108;
Conservative 0; Mismatches 62;
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B1 protein; intracellular mediator; modulator; inflammation; cell death; cell survival pathway; intracellular signalling; AIDS; cancer; human; ss
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cDNA encoding muri

S S Result

This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above cancer treating AIDS, 90pp; English for 3B; Fig 4 Claim

other σ ; H 539 : : C; 449 A; 452 BP; 649 Sequence 2098

pathways

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C77607 to C78448 encode the human cancer associated proteins given in B43398 to B44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antiasthmatic; antirherdic; antibacterial; antiviral; dermatological; antiapterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and vasotropic; antibodise, antibodises, and antiapoints from the present invention may be used to treat immune disorders by activating or invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of hamantopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection,
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acttcaaaataaaagcatgtaagtgactgttttcaagaagaaatgtgtttcataaaagg 1920
                                                                                                                                                                            Novel isolated nucleic acids comprising sequences encoding peptides
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or
modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. C78449 to C78457 and B44240 represent sequences used in the exemplification of the present
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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-8; SIDEP-1; DREP-1; diagnosis; cell growth; apoptosis dysregulation; que therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.
 2059
BP.
                                                                 CDNA; 2502
                                                                                                    Human RICK coding sequence.
                                                                                         (first entry)
                                                                 Z48762 standard;
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                        gaattt 2065
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tions for identifying apoptosis signalling pathway inhibitors for treating diseases $\boldsymbol{\cdot}$ WPI; 2000-072163/06. P-PSDB; Y59404. Compositions

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98US-0069023

27-APR-1999; 27-APR-1998;

04-NOV-1999

Homo sapiens W09955134-A2 (UNMI) UNIV MICHIGAN G, Inohara N,

Nunez

Claim 8; Fig 7b; 93pp; English.

This sequence encodes the human RICK (RIP-like interacting CLARP kinase)

C protein of the invention. The RICK protein acts as a positive regulator

C protein of the invention. The RICK protein acts as a positive regulator

C during CD95 signalling. The invention provides methods for identifying

apoptosis signalling pathway inhibitors and activators, and methods and

C compositions for screening compounds which will modulate the interactions

CC compositions compositions identified: ARC, RICK, and the CIDE family of

CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

assays for agents, useful in the diagnosis, prognosis or treatment of

disease associated with excess cell growth and dysregulation of

CC disease associated with excess cell growth and dysregulation of

CC disease associated with excess cell growth and dysregulation of

CC disease associated with excess cell growth and useful in Graph

CC apoptosis. Complexes containing RICK and CLARP can be used in drug

CC apoptosis. Overapression of ARC in an in vitro cell system can be used

CC identify inhibitors of the enzymatic activity of caspasae-8.

CC identification of ARC-like inhibitory compounds may be useful for gene

CC interapt reatment of disease with increased cell death in muscle tissue

CC can be used as reagents for the preparation or affinity chromatography

CC of an essential step in the blochemistry of apoptosis. A specific inhibitor

CC of an essential step in the blochemistry of apoptosis. A specific inhibitor

CC of an essential for apoptosis, inhibitors of RICK binding to intracellular

CC apoptosis factors are potential drug candidates.

S

Db 961 catcgacctgttat	1055	Oy 1115 tgtttaatagaact 	1175 gttattcago 	1235	Oy 1295 tgtggatcctctca 	Oy 1355 gctcctcaagacaa	Oy 1415 catcactgtcctgg	1475	. Qy 1535 ggaaactcagaacg 	Qy 1595 gacattgtgaacca 	1655	Qy 1715 aaagtcagacaatt 	Oy 1775 gtacaaaattgaa 	Qy . 1835 gittctagatcacc 	Oy 1895 caagaagaaatgtg 	Qy 1955 ataaaatccgtgag 	Oy 2015 ccatgacactgcag 	RESULT 4 Z46143
; 769 A; 535 C; 499 G; 699 T; 0 other;	95.7%; Score 2006.8; DB 21; Length 2502; ty 99.2%; Pred. No. 0; ervative 9; Mismatches 6; Indels 1; Gaps 1;	ggcaccagtctctagaaaagaagtcagctctggttcggagaagcagcggctggcgtgggc 95 	catcoggggaatgggcgccctcgtgacctagtgttgcggggcaaaagggtcttgccggc 155 	ctcgctcgtgcagggggtatctgggcgctgagcggcgtgggagccttgggagccgc 215 	cgcagcagggggcacacccggaaccggcctgagcgcccgggaccatgaacggggaggcca 275 	tetgcagcgccc-tgcccaccattccctaccacaaactcgccgacctgcgctacctgagc 334	cgoggogoctctggcactgtgtcgtccgcccgccacgcagactggcgcgtccaggtggcc 394		gaagctgaaatttacacaaagctagatttagttacatttttccaattttgggaatttgc 514 		ctcctacataggaaaactgaatatcctgatgttgcttggccattgagatttcgcatcctg 634 	catgaaattgccttggtgtaaattacctgcacaatatgactcctcttacttcatcat 694 	gacttgaagactcagaatatcttattggacaatgaatttcatgttaagattgcagattt 754 			gccagtatcaagcacgatatatagctatgcagttatcacatgggaagtgttatccaga 934		catcgacctgttattaatgaagaagtttgccatatgatatacctcaccgagcacgtatg 1054
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o Sequence	Query M Best Lo Matches	y 36 b 1	у 96 b 61	y 156 b 121	y 216 b 181	y 276 b 241	у 335 b 301	у 395 b 361	y 455 b 421	y 515 b 481	y 575 b 541	у 635 b 601	y 695 b 661	y 755 b 721	y 815 b 781	y 875 b 841	y 935 b 901	у 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baughn MR;
H, Azimzai Y;
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                                                                                                                                cDNA sequence encoding a human phosphorylation effector PHSP-6
                                                                                                                                                                        phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder; ss.
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Au-Young J, Gorgone GA, Yu
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/product= "phosphorylation effector"
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DAM, Shih
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P-PSDB; Y68774.
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Reddy R, Lu
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22-DEC-1998;
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Best_Local Similarity Matches 2002; Conserv

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Query Match

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CARD-3; caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
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This invention describes the isolation of novel human caspase
recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins of
recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins of
the invention are involved in the requisition of caspase activation.
The caspase recruitment domain (CARD) polynucleotides, polypeptides,
the chomologues and antibodies can be used in screening assays, detection
assays, predictive medicine and therapeutic and prophylactic methods of
treatment. The methods may be used to diagnose and treat patients which
complex, abnormal activity of the TNF receptor complex, or abnormal
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complex, and hormone-dependent tumours), autoimmune disorders (e.g. or
systemic lupus erythematosis, immune-mediated with mutations
complex, and hormone-dependent tumours), autoimmune disorders (e.g. or
systemic lupus erythematosis, immune-mediated glomerollonephritis), viral
complex, and sended in interacts with other cellular proteins, and so
can be used for regulation of cellular proliferation and differentiation
and call survival. The CARD proteins may also be used to for screen drugs
correction, which modulate their activity. The CARD-4 gene can express a
concounted which modulate their activity and CARD-4 gene can express a
concounted which modulate their activity and cARD-4 splice and express a
concounted which modulate their activity and cARD-4 gene can express a
concounted which modulate their activity in the methods.
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spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell survival
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroidiius; diabetes mellitus; Coron's disease; multiple sclerosis; rheumatoid arthritis; ulcerative collitis; cardiovascular disorder; wound healing; neurological disease; ds.
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Sequences F21614 - F22031 represent DNA sequences encoding human proteins B58711 - B59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences F22032 - F22040 and B59129 which are used in the isolation and craracterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive, nootropic; antiinflammatory; antiinles; immunosuppressive, nootropic; antiinflammatory; antiinles; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemats, wound healing; contrological and associated associated and associated and associated associated and associated associated associated associated and associated associated associated associated and associated as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 653; 1299pp; English.
                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                08-MAR-2000; 2000WO-US05881
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P-PSDB; B58938.
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The invention provides polynucleotides which encode novel protein kinase homologs expressed in various human cells and tissues. The present sequence represents the clone 156108 cDNA fragment derived from a human cDNA library designated THP-1 phorbol LPS. The cDNA encodes a protein kinase which shows homology to the U01064 Dictyostellum Y kinase. Vectors and host cells can be used for recombinant production of the protein kinase homology. The recombinant proteins may be used to raise antibodies for use as anti-kinase therapeutics. Oligonucleotides based on the polynucleotide sequences, i.e. probes and antisense constructs, the peptides and antibodies are claimed to be useful as tools for studying signalling cascades in cells and proteins, and for identifying inhibitors (drugs) to treat diseases and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions associated with abnormal kinase expression. Diseases that are claimed to be treatable include human X-linked agammaglobulinaemia, nonspherocytic haemolytic anaemia, artherosclerosis, carcinomas, diabetes, gliomas, restenosis, cholera-based septic shock, etc.
                                                                                                                                                                                                                                                                                                                                                        Protein kinase; cell signalling; inflammation; carcinoma; diabetes; human X-linked agammaqidobulinaemia; nonspherocytic haemolytic anaemia; artherosclerosis; glioma; restenosis; cholera-based septic shock; U01064 Dictyostelium Y kinase; ss.
                   965
                                                                                                                                                                                                                                                                                                                       Clone 156108 cDNA fragment encoding a human protein kinase homolog.
 cagttatcacatgggaagtgttatccagaaaacagccttttgaagatgtcaccaatcctt
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                                                                          tgcagataatgtatagtgtgtcacaaggacatcgacctgttat 1008
                                                                                            Sequence 210 BP; 74 A; 40 C; 41 G; 55 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-556387/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate anglogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle discretes. Sequences Zeinford from all process derived from all and an account of the sequences derived from all and account of the sequences derived from all accounts are sequenced and and account of the sequences derived from all accounts and account of the sequences derived from all accounts and account of the sequences derived from all accounts and account of the sequences derived from all accounts and account of the sequences derived from all accounts and account of the sequences derived from all accounts and account of the sequences derived from account of the sequences and account of the sequences derived from account of the sequences derived from account of the sequence and account of the sequence of 
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  embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; andyogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides useful for the treatment of various conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermal papilla; keratinocyte; neonatal foreskin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA encoding murine RIP protein kinase homologue, SEQ ID NO:403.
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                                                                                                                                                                                                     Claim 1; Page 228-229; 235pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
           Length 1774;
                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
                                               Indels
Score 102.4; DB 41;
Pred. No. 2.7e-11;
                                             0; Mismatches
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         1 4.9%;
Similarity 51.8%;
72; Conservative
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             Query Match
Best Local Sim:
Matches 372;
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                                                                                                                            Kumble KD, . Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 ctgcccaccattccctaccacaaactcgccgacctgcgctacctgagccgcggggcctct 346
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                                                                                                                                                                                                       New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
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ive 0; Mismatches 316; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1774 BP; 406 A; 490 C; 526 G; 352 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotides for examining expression patterns.
                                                                                                                            Onrust R, Sleeman M,
                                                                                                                                                                                                                                                                    Page 305-306; 352pp; English.
                                                                                            (GENE-) GENESIS RES & DEV CORP LTD
                             15-MAY-2000; 2000WO-NZ00075.
                                                             99US-0312283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 51.8 Matches 372; Conservative
                                                                                                                          Strachan L,
                                                                                                                                                       WPI; 2001-007495/01.
                                                                                                                                                                           P-PSDB; B56062
                                                             14-MAY-1999;
23-NOV-2000.
                                                                                                                            Watson JD,
                                                                                                                                                                                                                                                                      Claim 1;
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The present sequence encodes a murine death associated kinase protein, containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides can be used to express the polypeptides, and as probes to identify on ucleic acids encoding proteins having kinase activity. DAKAR polypeptides and fragmented polypeptides are used for purifying polypeptides and fragmented polypeptides are used for purifying proteins, e.g. to measure protein activity; as quality assurance agents to monitor shelf life and stability of binding partner proteins; as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds which may interfere with apoptosis; as molecular weight and isoelectric focusing markers; as controls for peptide fragmentation; identification of unknown proteins, controls for peptide fragmentation; identification of unknown proteins, and to purify the protein by immunoaffinity of the protein, and to purify the protein by immunoaffinity characteraphy. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity characteraphy. The antibodies can also be used to block binding of the DAKAR polypeptides to their binding partners. Compounds that inhibit or enhance the kinase activity of DAKAR can be used to treat diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel death associated kinase containing ankyrin repeats (DAKAR) used as molecular weight marker and as controls for peptide fragmentation
                                                                                                                                                                 947 gaagatgtcaccaatcctttgcagataatgtatagtgtgtcacaaggacatcgacctg 1004
                                                                                                                                                                                         Death associated kinase protein containing ankyrin repeats; DAKAR; kinase; quality assurance agent; shelf life; marker; ss.
attatttatatgccacctgaaaactatgaacctggacaaaaatcaagggccagtatcaag
                                       558 atcgcttacctccctccagagcgaatt---cgtgagaagagccgcttgtttgacaccaaa
                                                                                cacgatatatatagctatgcagttatcacatgggaagtgttatccagaaaacagcctttt
                                                                                                      DNA encoding a death associated kinase with ankyrin repeats
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/*tag= a
/transl_except= (pos:10..12, aa:
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98US-0099973.
99US-0119353.
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P-PSDB; Y69163.
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11-SEP-1998;
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follicle disorder;

hair

anti-inflammatory; cytostatic; neuroprotective; vulnery;

developmental disorder; skin wound;

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                                                                                      DB 21; Length 2370;
   production or DAKAR.
                                                                                                                  Indels
                                          Sequence 2370 BP; 536 A; 660 C; 700 G; 474 T; 0 other;
                                                                                    Score 102.4; DB 21;
Pred. No. 2.9e-11;
0; Mismatches 316;
 characterized by overproduction or upregulated underproduction or downregulated production of
                                                                                   4.9%;
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                                                                                                  Best Local Similarity 51.8
Matches 372; Conservative
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characterized
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The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and translat amplifying calls. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences Z61606-Z61802 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences Z61606-Z61849, 261725-Z61765, Z61802-Z61811 and Z61826 encode proteins with an sequence, indicating that the proteins are secreted. Sequences Z61650-Z61668, Z61766-Z61810, Z61812-Z61817 and Z61812-Z61817.

Murison JG;

Onrust R, Kumble A,

Watson JD,

Sleeman M,

Strachan L,

WPI; 2000-072177/06 P-PSDB; Y76079

(GENE-) GENESIS RES & DEV CORP

99WO-NZ00051 98US-0069726.

29-APR-1999; 29-APR-1998; 09-NOV-1998;

04-NOV-1999

WO9955865-A1

Mus

Novel polynucleotides useful for the treatment of various conditions including wounds and cancer -

235pp; English.

Claim 1; Page 158-159;

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Gaps

30;

Length 3516;

Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other;

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43 ctgcgcaccttcgacgccggcgaattcgcaggctgggagaaggtgggctcggggcttc 102
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Score 102.4; DB 21; Length
Pred. No. 3.2e-11;
0; Mismatches 316; Indels
4.9%;
51.8%;
Query Match
4.99
Best Local Similarity 51.89
Matches 372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA encoding murine protein kinase/ankyrin homologue, SEQ ID NO:257
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27-MAR-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murison JG;
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                                                                                                                                                                                                                                                                            New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
         cttggtgtaaattacctgcacaatatgactcctctttacttcatcatgacttgaagact
                                 382 gigggeatgaacticcigcattgeatgictecgecactgeacctagaccigaageca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttacacaaagctagatttagttacatttttccaattttgggaatttgcaatgagcctgaa
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                                                                                                         Length 3516;
                                                                                                                                                 30;
                                                                                                                                                 Indels
                                          Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other;
oligonucleotides for examining expression patterns.
                                                                                                           DB 22;
                                                                                                    Score 102.4; DB 22;
Pred. No. 3.2e-11;
0; Mismatches 316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene signature HUMGS00852.
                                                                                                       Query Match
Best Local Similarity 51.8%;
Matches 372; Conservative
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11-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA) which comprises one of the 7837 "6S" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end translated sequence is unique to a particular mRNA species, almost all the 3'-oriented comas hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fel; protein kinase; mouse; signal transduction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 108 BP; 36 A; 14 C; 13 G; 39 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 3..2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 469; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258584 standard; cDNA; 2294 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse protein kinase Fel cDNA.
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                                                                                                                                                                                                                                 (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-206931/27.
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Matches 102; Conserv
                                                                                                                                                                                                                                                         OKUB/) OKUBO
                                                                                                                                                                                                                                                                                                        Matsubara K,
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                                                                                                                                                                               12-NOV-1993;
                            W09514772-A1
                                                                                 01-JUN-1995
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The present sequence is that of Genesis clone 971025TRAM004820HT

(Fel) DNA. The translation of the clone (frame 3) is provided in cry91s4. The polypeptide has kinase activity. The invention relates to purified murine polypeptides (see Y79152-56) that have kinase function and isolated nucleic acids encoding them (see CS5882-86). The nucleic acids can be used to express the polypeptides, as probes to identify nucleic acids encoding proteins polypeptides, as probes to identify nucleic acids encoding proteins having kinase activity, and in assays to identify chromosomes, map murine genes, and study tumours. Vectors comprisaing the novel nucleic acids and host cells (bacterial, yeast, plant, insect or animal) transfected or transduced with the vectors are claimed. The kinase polypeptides and their fragments are used as mol.wt. and isoelectric focusing markers, and as controls for peptide isoelectric focusing markers, and as controls for peptide kinases play a central role in cellular signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel murine polynucleotides encoding kinase polypeptides, used a probes to identify nucleic acids encoding proteins having kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30:
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                                                                                                                                                                                                                                                               Marken JS;
                                                                                                                                                                                                                                                               Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 3; 93pp; English
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ilarity 51.9%;
Conservative C
                                                                   98US-0095269
98US-0099973
99WO-US17577
                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                               Virca GD, Bird TA,
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P-PSDB; Y79154.
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Matches 350; Conserv
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Length 3033;

Query Match

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750 attttggtttatcaaagtggcgcatgatgtccctctcacagtcacgaagtagcaaatctg 809
                                  cacagaagaagccatttgcagatgaaaagaacatcctacacatcatgatgaaagtggtaa 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The CTR1 gene was mapped to an interval between 2 RFLPs in chromosome 5 of A. thaliana and a chromosome walk in this area was initiated using a YAC library, 2 clones were isolated and used to probe a cDNA library derived from polyA RNA from 3 day-0ld dark-grown, ethylene-treated A. thaliana seedlings. The cDNA for the CTR1 gene is given in Q98816. Expression of the CTR1 gene in transgenic plants results in a dominant ethylene-insensitive
                                                                                                                  810 caccagaaggaggacaattatttatatgccacctgaaaactatgaacctggacaaaat
                                                                                                                                                           constitutive triple response; transgenic plant; ethylene; stolerance; crop improvement; ss.
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AVKHLHIHTPLLDSERKDVLREAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
LIBELLHKRYEPEPVAMPLERAILHEIALGYMYLHMYEPPLHHDLKYQUILLDNEFHV
KIABLGISKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEPGKSRASIKHDILKDNEFHV
TWEVLSKQPFEDYNPRLQIMYSVSQGHRPYINEESLDYDIHRARMISLIESGWAQN
PDERSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLN
SWDSTISGSQRAAFCHHKTPGSSAIENSLAFSKSLAPAODNELSKRAADOYFWKLHCPGNH
SWDSTISGSQRAAFCHKTTPCSSAIINPLGTAGNSBRLQPGIAQQMIQSKREDIVN
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Arbor,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2501)
Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
RICK, a novel protein kinase containing a caspase recruitment
domain, interacts with CLARP and regulates CD95-mediated apoptosis
J. Biol. Chem. 273 (20), 12296-12300 (1998)
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Inohara, N., Koseki, T., Chen, S., del Peso, L. and Nunez, G.
Direct Submission
Submitted (01-0CT-1997) Dept. Pathlogy, Comprehensive Cancer
Geriatrics Center, 4-131 CGGC 1500 E. Medical Center Dr. Ann
MI 48109, USA
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/note="CARD domain protein; phosphorylated
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="GI:3123887"
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225. .1847
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Octa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; lia; Eutheria; Primates; Catarrhini; Hominidae; Homo. sees 1 to 1902)
,M., Hofmann,K., Burns,K., Martinon,F., Bodmer,J.-L., ann,C. and Tschopp,J.
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Biol. 8 (1998) In press
sises 1 to 1902)
M., Hofmann, K., Burns, K., Martinon, F., Bodmer, J.-L.,
Inn, C. and Tschopp, J.
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243. .1865
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                                                                                                                                                domain"
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1125. .1544
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1545. .1811
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Pred. No. 0;
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sapiens"
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1545. 1811
/note="encodes CARD m
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Best Local Similarity 99.6
Matches 1861; Conservative
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McCarthy, J.V., Ni, J. and Dixit, V.M.
RIP2 is a novel NF-kapaB-activating and cell death-inducing kinase J. Biol. Chem. 273 (27), 16968-16975 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="RIP2"
/function="activtes NF-kappaB"
/function="induces cell death"
/note="RIP2; serine/threonine kinase
CARD motif"
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Pred. No. 1.8e-277;
0; Mismatches 4;
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/gene="RIP2"
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1 (bases 1 to 116650)
Ozersky, P., Holmes, A. and Broy, M.
The sequence of Homo sapiens BAC clone CTA-437L15
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                                                                                           cctacaaggacctcaaaagtcagacaattactagacactactgacatccaaggagaagaa 1759
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                                               tattttatgaagctgcatcactgtcctggaaatcacagttgggatagcaccatttctgga 1459
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Park Avenue, St. Louis,
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Park Avenue, St. Louis,
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Homo sapiens BAC clone CTA-437LL5
AC004003
MC004003.1 GI:2772557
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University, 4444 Forest
4 (bases 1 to 116650)
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University, 4444 Forest
3 (bases 1 to 116650)
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Waterston, R.
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/rpt_f.gnlly="Alu"
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7110. 8040
710. 40218
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36395. 36488,39123. 39284,39881. 40218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
Clone CTA-437L15 is from a release of the human BAC library
CITB-HS-A. The library contains cloned DNA from human sperm. See:
Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J.
Shizuya et al., Genomics 34:213-8 (1996). The clone is available from
Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                          the entire insert of this
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                                                                                                                                                                                         clone sections once, or longer because we only sequence overlapping between neighboring data submissions.
                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The clone sequenced to the left is CTA-237G1. The actual start of this clone is at base position 1 of CTA-437L15; actual end is at 116650 of CTA-437L15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmmc.org) at the Virginia Mason Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone contains STS HS275YF1 (NID:g1051703).
Location/Qualifiers
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/db_xref="taxon:9606"
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
..... Summary Statistics
                                                                                                                                                                          NOTICE: This sequence may not represent
                                                                                   Center project name: H_RG437L15
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3188. .3340
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gigaaccaaaigacagaagceigectiaaccagicgeiagaigeeeiteigicaagggae 1660
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AF117829 320250 bp DNA
Homo sapiens 8q21.3: RICK gene, complete sequence.
AF117829.1 GI:4151947
HTG.
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Pred. No. 3.7e-82;
9; Mismatches 3; I
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                                                                           LNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHV
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331.5. .3328.

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A., Rowitch, D. and Pillai, S.
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Au-Young, J., Bandman, O., Hawkins, P.R.
Human kinase homologs
Patent: US 5817479-A 31 06-OCT-1998;
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AR044139
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/rpt_family="THE1C"
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QKRPPADEKNILHIMMKVVKGHRPELPPICRPRACASLIGLMQRCWHADPQVRPTF
QETISFEDEDLCEKPDEEVKDLAHEPGEKSSLESKESRRERSSRIKRASAPPFDNDCSL
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FEREASTGDLGFPDIQKKKLVDAIISGDTSRLMKILQPODVDLVLDSSASLLHAVEA
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KTWLAIKCSPSLHVDDRERMELLEBAKKMEMAKFRYILPVYRICQEPVGLVMEYMETG
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Direct Submission
Submitted (01-28P-2000) Cancer Center, Massachusetts Genera
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
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    3559
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LLGOLDSGYSGACHERSSSESKLPSSGSGKRLSGVSSVDSAFSSRGSILSLSF
REPSTSDLGTTDVQKKKLVDAIVSGDTSKLMKILQPQDVDLALDSGASLLHLAVEAGQ
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Bahr,C., Rohwer,A., Stempka,L., Rincke,G., Marks,F. and Gschwendt,M. Bir, a Novel Protein Kinase That Interacts with Protein Kinase Cdelta. CLONING, CHARACTERIZATION, AND GENE ANALYSIS
J. Biol. Chem. 275 (46), 36350-36357 (2000)
cacgatatatatatctatgcagttatcacatgggaagtgttatccagaaaacagcctttt 946
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Submitted (18-MAY-2000) Gschwendt M., Blochemistry of
Tissue-specific Regulation, German Cancer Research Center,
Neuenheimer Feld 280, D-69151 Heidelberg, GERMANY
Location/Qualifiers
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3838. .3843
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Homo sapiens mRNA for protein kinase (dik gene).
AJ278016
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/db_xref="taxon:9606"
/clone_lib="HaCaT"
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                                                 ctgcccaccattccctaccacaaactcgccgacctgcgctacctgagccgcgggcgctct 346
                                                                       CIGCGCACCITCGACGCGGCGAGITCACGGGTGGGAGAAGGIGGGCTCGGGCGTTC 147
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 DB 92;
                         0; Mismatches 319;
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Ecker,J.R. and Kieber,J.J.
Constitutive triple response gene and Patent: US 544166-A 1 22-AUG-1995;
Location/Qualifiers
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Pred. No. le
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Sequence 1 from patent US 5444166.
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114046.1 GI:996469
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 4.78;
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             Best_Local Similarity 51.4
Matches 369; Conservative
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                                                                            1808 CIGTCCACCGTGAGTGGCATGGTTGGTTGCTGTGAAAATTCTCATGGAGCAAG 1867
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                                                      ecgecegecacgeagactggegegtecaggtggeegtgaageacetgeacatecacaete 419
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Unclassified.

E 1 (bases 1 to 3033)

KS Ecker,J.R. and Kleber,J.J.

AL Patent: US 5602322-A 1 11-FEB-1997;

Location/Qualifiers

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Pred. No. 7.6e-05;
0; Mismatches 201;
                            Mismatches 201;
 DB 10;
 Score 81.4; DB 10 Pred. No. 7.6e-05,
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Sequence 1 from patent US 5602322
135764 1 GI:2087615
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Best Local Similarity 50.1%;
Matches 202; Conservative
3.9%;
Similarity 50.1%;
32; Conservative
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Best Local (
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VICTAINSTACT TO THE WORK OF THE WOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ethylene response pathway; negative regulator; protein kinase. Arabidopsis thaliana (strain Columbia) dark grown seedling (3 days old) hypocoryl and cotyledon cDNA to mRNA.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicoryledons; core eudicots; Rosidae; eurosids II; leassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEYLSRGSLYRLLHKSGAREQLDERRRLSMAYDVAKGMNYLHNRNPPIVHRDLKSPNLL
LYDKKYTWYCDFGLSRLKASTFLSSKSAAGTPEWMAPEVLRDEPSNEKSDVYSFGVI
LWELATLQOPWGNLHRAQVVARVGFKCKRLEIPRNLNPQVAAIIEGCWTNEPWRRPSF
ATIMDLLRPLIKSAVPPPNRSDL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATHCTRIA 3033 bp mRNA PLN 27-APR-1993 Arabidopsis thaliana negative regulator of the ethylene response pathway (CTR1) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                    2108 ATCTTCACAATCGCAATCCTCCAATTGTGCATAGAGATCTAAAATCTCCAAACTTATTGG 2167
                                                                                                                                                                                                                                                           660 acctgcacaatatgactcctctttacttcatcatgacttgaagactcagaatatcttat 719
540 ttactgaatacatgccaaatggatcattaaatgaactcctacataggaaaactgaatatc 599
                                                                                                                          600 ctgatgttgcttggccattgagatttcgcatcctgcatgaaattgcccttggtgtaaatt
                                                                                                                                                                      1988 TGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGG
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/dev_stage="dark grown seedling (3 days old)"
/tissue_type="hypocotyl and cotyledon"
118. .2583
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/strain="Columbia"
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/protein_id="AAA32779.1"
/db_xref="GI:166680"
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/gene="CTR1"
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TITLE
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MEDLINE
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Score 81.4; DB 13; Length 3033; Pred. No. 7.6e-05;

3.9%; 50.1%;

Best Local Similarity

Query Match

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AF110519 2767 bp mRNA PLN 28-JAN-1999
Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase
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| protein_id="AAD10057.1"
| db_xref="G1:4193950"
| /translation="MSGRRSSYTLLNQIPNDNFFQPPAPKFSAGAGVLPYGESSSAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRGKVFDLDLMDQRMMQSHNRVGSFRVPGSJGSQKQSTEGSFRGSSLSGENYVGTSFG
HKNEGCGSSVRNWAQQTEESYQLQLALAIRLSEATCADSPRFLDPYTDVLASRDSD
STASAVTMSHRLMINGCMSYFDKVPDGFWIYGMDPYWALCSVVQESGRIPSIESLK
AVDPSKAAPSVEVILIYTYCNDLJSLKECONRIHSISPGCITTKEAVDQLAKLVCDHMGGA
APAGEEELVSMSKGCSNDLKDRFGTIVLPIGSLSVGLCRHRALLFRVLADIIDLPCRI
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Kannan, P. and Glovannoni, J.J.

Direct Submission
Submitted (02-DEC-1998) Horticultural Sciences, Texas A&M
University, Mail Stop 2133, College Station, TX 77843-2133, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2047
                                                                                                                                                                             1928 GCCACCCTAACATTGTTCTTTCATGGGTGCGGTCACTCAACCTCCAAATTTGTCAATAG 1987
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                                                               1808 CIGICCACCGTGCTGAGTGGCATGGCTCGGATGTTGCTGTGAAAATTCTCATGGAGCAAG 1867
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360.ccgcccgccacgcagactggcgcgtccaggtggccgtgaagcacctgcacatccacactc 419
                                                                                                                                   420 cgctgctcgacagtgaaagaaaggatgttttaagagaagctgaaattttacacaaagcta
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Kannan, P. and Glovannoni, J.J.

Ethylene-inducible tomato CTR1-like protein kinase
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/organism="Lycoperstoon e:
/organism="Accoperstoon e:
/oultivar="Allsa Craig"
/db.xref="taxon:4081"
/chromosome="2"
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/db_xref="taxon:4081"
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AKGCKYCNSSDASSCLVRFEHDREYLVDLIGKPGVLSEPDSLVNGPFSISIPSPLRFP
RYRQVEPTTDFRAAADGDAGQSDRSCIDRNNVVSSSSNRDEISQLPPPPLNAWKKGRD
KESQLSKMYNPRSMLNPVNMDEDQVLVKHVPPFREDAQSPMTRPDTVNDTRFLAGGGH
                                                         VVSÅI PSEELDLDVEEFNI PWNDLVIMEKIGAGSFGTVHRGDWHGSDVAVKIIMEQDF
HAERLKEFIREVAIMKRLRHPNIVLFWGAVIQPPNLSIVTEYISRGSLYRLLHKPGAK
KVLDERRPLCLAYDVANGMNYLHKRNPPIVHRDLKSPNILVDKKYTVKICDFGLSRFK
                                                                                                                  ANTFLSSKTAAGTPEWMAPEVIRDEPSNEKSDVYSFGVILWELATLQQPWNKLNPPQV
IAAVGFNRKKLDIPSVLNPRVAIIIEACWANEPWKRPSFSTIMDMLRPHLKSPLPPPG
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Lycopersicon esculentum ethylene-responsive protein kinase TCTR1
(ERR5) mRNA, complete cds.
AF0965250 GI:5669641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-OCT-1998) Lab 'ETHYLENE', ENSAT-INRA, Avenue de 1'Agrobiopole BP 107, Auzeville Tolosan, Castanet Tolosan cedex 31326, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1780 AAGGAATTTTTGAGGGAGGTTGCAATTATGAAGCGGTTGCGACATCCAAATATTGTACTT 1839
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                                                                                                                                                                                                                                                                                                                                     440 aaggatgitttaaggagagcigaaattitacacaaagciagattiagtiacattiticca 499
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1. .2829
/organism="Lycopersicon esculentum"
/cultivar="Evita"
                                                                                                                                                                                                                                                      Score 78.2; DB 12;
Pred. No. 0.00028;
0; Mismatches 153;
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2080 AAGATCTGTGATTTTGGTCTTTC 2102
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52.6%;
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source

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AF110518 2836 bp mRNA PLN 28-JAN-1999 Lycopersicon esculentum ethylene-inducible CTR1-11ke protein kinase mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ethplene-responsive protein kinase TCTR1"
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STASAYTMANNGWASTPSTKPORYDFORFYNTOMDPYWALCSVVQESGRIPSIESLR
AVDPSKAPSYLLINGKNDISLELKELQNRIHSISPSCITTKEAVDAIDLDPCRI
ARGCKYCCNSCASASSCIVYFEHDREYLVDLIGFGSLSVGLCRHRALLFRVLADIIDLPCRI
AKGCKYCCNSSASSCIVYFEHDREYLVDLIGFGSLSVGLCRHRALLFRVLADIIDLPCRI
AKGCKYCCNSSASSCIVYFEHDREYLVDLIGFGSLSVGLCRHRALLFRVLADIIDLPCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSTYTEYLSRGSLYRLLHKPGAREWLDERRRCCMAYDYANGMNYLHKRNPPTYHRDLK
SPNLLVDKKYTVKICDFGLSRFKANTFLSSKTAAGTPEWMAPEVIRDEPSNEKSDVYS
FGVILWELATLQOPWNKLNPPQYIAAVGFNRKRLDIPSDLNPQVAIIIEACWANEPWK
RPSFSTIMDMLRPHLKSPLPPPGHTDMQLLS*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYRQVEPTTDFRSLAKQYFLDSQSLNLLFDDSSAGAAADGDAGQSDRSCIDRNNVVSS
SSRDEBISQD-PLANAKKGRNKESQDLSKMYNRESMINPWNDEDQVVKHVPPFRE
SAGSPWTRPDTVNDTRFLAGGGHVSA.IPSEELDLDVEEFNIFWNDLILMEK GAGSF
GTVHRGDWHGSDVAVKILMEQDFHAERLKEFLREVAIMKELRHPNIVLEMGAVIQPPN
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                                                                                                                                                                                                                                                                                                                        /note="serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1835 AAGGAATTTTGAGGGAGGTTGCAATTATGAAGCGGTTGCGACATCCAAATATTGTACTT 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 attitigggaatttgcaatgagcctgaatttttggggaatagttactgaatacatgccaaat 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 aaggatgiiitaagagaagcigaaaiiittacacaaagciagaiitagiiacaiiiticca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 agatttcgcatcctgcatgaaattgcccttggtgtaaattacctgcacaatatgactcct
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Pred. No. 0.00028;
0; Mismatches 153;
/tissue_type="green fruit"
/dev_stage="late immature"
/note="ethylene-treated"
                                                                                                                                                            /note-"ethylene-inducible"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          845
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/gene="ER50"
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                                                                                                                                                                                                                                                                                             /gene="ER50"
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Matches 170; Conservative
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AF110518
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APAGEELVSMSKGCSNDLKDRFGTIVLPIGSLSVGLCRHRALLFKVLADIIDLPCRI
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DAQSPMTRPDYVNDTRLAGGGHVVSA LYSEELDLDVEEFNIFWNDLVLMEK GAGSF
GTVHRGDWHGSDVAVKILMEQDFHAERLKEFLREVAIMKRLRHPNIVLLMEK GAGSF
                                                                                                                          Eukaryota; Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Solanales; Solanaceae; Solanum; Lycopersicon.

I (bases 1 to 2818)

Kannan, P. and Glovannoni, J.J.

Ethylene-inducible tomato CTR1-like protein kinase
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/note="protein kinase homolog; ethylene and fruit ripening
inducible CTRI-like protein kinase; TCTRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSIVTEYLSRGSLYRLLHKPGAKKVLDERRPLCLAYDVANGMNYLHKRNPFIVHRDLK
SPULLVDKYTYVICDFGLSRFKANTFLSSKTRAGTPEWMAPEVIRDEPSNEKSDVYS
FGVILWELATLQOPWNKLNPPQVIAAVGFNRKKLDIPSVLNPRVAIIIEACWANEPWK
RPSFSTIMDMIRPHLASPLPPGGHTDMOLLS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRGKVFDLDLMDQRUMQSHNRVGSFRVPGSIGSQKQSTEGSFRGSSLSGENYVGTSFG
HKNEGCGSSVARNWAQQTEESYQLQLALAIRLSSEATCADSPNFLDPVTDVLASRDSD
STASAVTMSHRLWINGCMSYFDKVPDGFYWIYGMDPYWALCSVVQESGRIPSIESLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVDPSKAPSVEVILIVRCNDLSLKELQNRIHSISPSCITTKEAVDQLAKLVCDHMGGA
                                                                                                                                                                                                                                                                                                    2 (bases 1 to 2836)
Kannan, P. and Giovannoni, J.J.
Direct Submission
Submitted (02-DEC-1998) Horticultural Sciences, Texas A&M
University, Mail Stop 2133, College Station, TX 77843-2133, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="ethylene-inducible CTR1-like protein kinase"
/protein_id="AAD10056.1"
/db_xref="GI:4193948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1909 TTTATGGGTGCTGTCATTCAGCCACCAAATTTGTCCATAGTCACGGAATATTTATCGAGA 1968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1849 AAGGAATTTTTGAGGGAGGTTGCAATTATGAAGCGGTTGCGACATCCAAATATTGTACTT 1908
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/organism="Lycopersicon esculentum"
/orlitvar="Allsa Craig"
/db_xref="taxon:4081"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score 78.2; DB 12;
illarity 52.6%; Pred. No. 0.00028;
Conservative 0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="between TG33 and CT106A"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                     Lycopersicon esculentum
     AF110518
AF110518.1 GI:4193947
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Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                               Unpublished
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                                                                              tomato.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
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AUTHORS
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Oy 740 aagattgcagattttggtttatc 762 | Oy 140 aagattgcagattttgfttatc 762 | Op 2149 AAGATCTGTGATTTTGGTCTTTC 2171
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Search completed: June 13, 2001, 17:39:55 Job time: 9374 sec

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Appli Appli Appli

Sequence Sequence

Sequence Sequence

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Sequence 5, A Sequence 10, Sequence 6, A Sequence 6, A Sequence 6, A Sequence 6, A Sequence 11, Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 25 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DIskette
COMPUT
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99.6%; Pred. No. 1.5e-260;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                DCT-US95-05088-10
US-08-701-191A-37
US-09-035-706-6
US-08-955-841-6
US-08-571-758-11
                                                                                                                       US-08-473-553A-5
US-08-587-889-2
US-08-980-060-5
US-09-307-185-5
PCT-US96-09193-2
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US-08-909-983-11
US-08-587-680A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09019942
Patent No. 6033855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., An:
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                        SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
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APPLICANT: Steamen, Lorna
APPLICANT: Steamen, Matthew
APPLICANT: Steamen, Matthew
APPLICANT: Oncust, Rene
APPLICANT: Oncust, Rene
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 334, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
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LENGTH: 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EG--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV
                                                  G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 536; DB 4; Length 536;
; Pred. No. 8.9e-43;
64; Mismatches 159; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Stream, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Ornust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 185, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| : |:| : ::|
429 LQPQDVDLVLDSSASLLHLAVEA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 IQSKREDIVNQMTEACLNQSLDA
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Best Local Similarity 32.5%;
Matches 164; Conservative 64
                                                                                                                                                                                                                                                                                                                                          361 SRSLPAPQDNDF------
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GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL 142
                                                                                                     249 VINE--ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEP-VLRTFEEITFLEA 305
                                                                                                                                                                                                                                                                                                                      306 VIQLKK-----TKLQSVSSAIHLC------DKKKMELSLNIPVNHGPQEESCGSSQ 350
                                                                                                                                                                                                                                                                                                                                                                                                 351 LHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHK 410
                                                                                                                                                                                                                                                                                                                                                                                                                          71 HKARFSYIFPILGICNEPEF----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRIL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFWENGSLSGLLQSQCPRP---WPLLCRLL 121
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                                                                                                                                                             194 PPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRP
                                                                                                                                                                                      302 VASLKKEYPDOSPVLQRMFSLQHDCVPLPPSRSNSEQPGSLHSSQGLQMGPVEESWFSS-
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                                                                                  143 LHHDLKTQNILLDNEFHVKIADFGLSKWRMMS-LSQSRSSKSAP-----EGGTIIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 518;
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ilarity 25.7%; Pred. No. 9.1e-29;
Conservative 84; Mismatches 183;
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APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REPERENCE: PHM. 70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09329418 Patent No. 6096539
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Best Local Similarity
Matches 132; Conserv
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US-09-329-418-9
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                                                                                                                      ---LSRKAQDCYFMKL-----HHCPG 390
                                       300 ITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPE 359
                                                                            ---SETEDLCEKPDEEVK---DLAHEPGEKSSLESKSEARPESSR 321
                                                                                                                                                                                                                                   379 VSSVDSAFSSRGSLSLSFEREASTGDLGPTDIQKKKLVDAII-----SGDTSRL----M 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 LKRASAPPFDNDCSLSELLSQLDSGIFPRLLKGPEELSRSSSEC---KLPSSSSGKRLSG
                                                                                                                                                                                                  ----CDHKTTPCSSAIINPLSTAGNSERLQPGIAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPART: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005
239 VKGHRP----ELPPICRPRARACASLIGLMQRCWHADPQVRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00383/026001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Leder, Philip
APPLICANT: Seed, Brian
APPLICANT: Stanger, Ben Z.
APPLICANT: Lee, Tae-Ho
APPLICANT: Kim, Emily
TITLE OF INVENTION: CELL DEATH PROTEIN
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                           438 QWIQSKREDIVNQMTEACLNQSLDA 462
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08444005
Patent No. 5674734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul T.
REGISTRATION NUMBER: 00.164
REFERENCE/DOCKET NUMBER: 0038
TELECOMMUNICATION INFORMATION:
TELEPPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                      KILQPQDVDLVLDSSASLLHLAVEA
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INFORMATION FOR SEQ ID NO: 15:
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LENGTH: 656 amino acids
                                                                                                                    360 TSRSLPAPQDNDF-----
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                                                                              281 IT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLDNEFVLRLEGVIEKVGGSSQDPK-PALVTKFMENGSLSGLLQSQCPRP---WPLLCR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 HKARFSYIFPILGI-----CNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFR 123
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                                                                                                                                                                                                                                                                                                                                                                                                   184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Dominant Negative Mutant Embodiment US-09-329-418-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.6%; Score 385; DB 3; I
Best Local Similarity 31.7%; Pred. No. 2.2e-28;
Matches 101; Conservative 63; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA LIMITEd
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
                                                                                                                                                                                                                                                                                                                                     Mismatches 123;
                                                                                                                                                                                                                                                                                          Score 386.5; DB 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 518
FILE REFERENCE: PHW.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 420
                                                                                                                                                                                                      ; OTHER INFORMATION: Delta Death Domain US-09-329-418-8
                                                                                                                                                                                                                                                                                            13.7%; Scc
32.1%; Pre
tive 62;
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                                                                                                                                                                                                                                                                                                                                     Matches 103; Conservative
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Best Local Similarity
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US-09-329-418-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 GHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEIT 301
                             ----- LCDKKKMELSL 333
                                                                      354
                                                                                                                                                                                              -----FMKLHHCPGNHSWDSTISGSQRAAFC 407
                                                                                                                                                     EEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPETSTFRNQMPSPTST 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 PTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEIL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 EGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQ
                                                           Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
ITTLE OF INVENTION:
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 388; DB 3; L
llarity 32.0%; Pred. No. 1.1e-28;
Conservative 62; Mismatches 125;
                                ---TKLQSVSSAIH--
                                                                                                                                                                                                                                                                               DHKTTPCSSAIINPLSTAGNSERLQ--PGIAQQ 438
                                                                                                                                                                                                                                                                                                       470 --QTTALPTAGLAP---SGKGRGLQHPPPVGSQ 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-05-329-418-8; Sequence 8, Application US/09329418; Patent No. 6096539
                                                                                                                                                                                                362 -RSLPAPQDNDFLSRKAQDCY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo Sapiens
US-09-329-418-3
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Best Local Similarity
Matches 102; Conservat
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LENGTH: 518
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Length 518; Indels S

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520 MNAPPISQPVPNRANRELGLDGDDMDIPW---CDLNIKEKIGAGSFGTVHRAEWHGSDVA 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IPYHKLADLRYLSRGASGTVSSARHADWR-VQVA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 821;
                                         APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Mismatches 111; Indels
                                                                                                                                                           ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,464
FILING DATE: 19920810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 376; DB 1; 30.7%; Pred. No. 3.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UPN-1086
                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Polician
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-003-311B-2; Sequence 2, Application US/08003311B; Patent No. 5444166; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
TOPOLOGY: 11.
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Best Local Similarity 30.7
Matches 98; Conservative
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793 WKRPSFATIMDLLRPLIKS
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                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNGEAICSALPT--
                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 19103
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ASLDNEFVLRLEGVIEKVNWDQDPRPALVTKFMENGSLSGLLQSQCPRP---WPLLCRLL 121
                                                                               186 EGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQ 244
                                                                                                                                                                                                                                          71 HKARFSYIFPILGICNEPEF----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRIL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 PTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEIL 70
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                                                          HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP
                                                                                                                                                               180 -GGTLGYLAPELF-VNVNRKASTASDVYSFGILMWAVLAGRE-VELPTEPSLVYEAVCNR
                                                                                                                                                                                                                   GHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09329418

Patent No. 6096539

GENERAL INFORMATION:
APPLICANT: ZENEZ LIMITEd

TITLE OF INVENTION:
FILE REFERENCE: PHM. 70536

CURRENT APPLICATION NUMBER: US/09/329,418

CURRENT FILIG DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 380; DB 3; L
ilarity 31.7%; Pred. No. 6.6e-28;
Conservative 62; Mismatches 126;
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US-07-928-464-2
; Sequence 2, Application US/07928464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                 302 FLEAVIQLKKTKLQSVSSA 320
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Best Local Similarity
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LENGTH: 518
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Matches 101;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 821;
         TITLE OF INVENTION: Constitutive Triple Response Gene TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORPERSON:
                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: No. 5444166ris
STREET: One Liberty Place - 46th Floor
CITY: Phlladelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 376; DB 1; Le 30.7%; Pred. No. 3.2e-27; Live 60; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
FILING DATE: AUGUST 10, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lori Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3109
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-261-432-2
; Sequence 2, Application US/08261432
APPLICANT: Kieber, Joseph J. TITLE OF INVENTION: CONSTITUTION: and Muta
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 821 amino acids
TYPE: amino acid
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                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-003-311B-2
                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 98; Conserva
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520 MNAPPISQPVPNRANRELGLDGDDMDIPW---CDLNIKEKIGAGSFGTVHRAEWHGSDVA 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNGEAICSALPT------IPYHKLADLRYLSRGASGTVSSARHADWR-VQVA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
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30.7%; Pred. No. 3.2e-27;
.tve 60; Mismatches 111; Indels
                                                                         Constitutive Triple Response Gene
                                                                                                                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5603322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
                                                                                                  and Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGORALIA MANER LOTI Y. BEATGELL REGISTRATION NUMBER: 34,293 REFERENCE/DOCKET UNBER: UPP TELECOMMUNICATION INFORMATION: 215-568-3100
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 DERPSFLKCLIELEPVLRT 296
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793 WKRPSFATIMDLLRPLIKS 811
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 13.39
Best Local Similarity 30.77
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-432-2
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                         NUMBER OF SEQUENCES:
                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                       19103
19103
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                                                                                                                                                                                                                                                                                         COUNTRY:
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12;

10;

Gaps

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52 VLRLEGVIEKVNWDQDPKPALVTKFMENGSLSGLLQSQCPRP---WPLLCRLLKEVVLGM 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQGHRPVIN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 IFPILGICNEPEF----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGV 132
                                                                                                                                                                                                                                                                                                                                                                                                                    18 LADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEILHKARFSY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103; Indels
                    APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 EESLPY - - - DIPHRARMISLIESGWAQNPDERPSFLKCL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dedhar, Shoukat
APPLICANT: Hannigan, Greg
TITLE OF INVENTION: Integrin-Linked Kinase and
TITLE OF INVENTION: its Uses
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   13.1%; Score 372; DB 3; 34.1%; Pred. No. 1.3e-27; ive 53; Mismatches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Bozicevic & Reed, LLP
285 Hamilton Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: LEGICAL DOS
OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                  CURRENT APPLICATION NUMBER: US/09/329,418 CURRENT FILING DATE: 1999-06-11 NUMBER OF SEQ ID NOS: 39 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 6 LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09035706
Patent No. 6001622
                                                                                                                                                                                                                                              ) OTHER INFORMATION: Kinase Domain US-09-329-418-6
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherwood, Pamela
                                                                                                                                                                                                                                                                                                                                     Query Match 13.19
Best Local Similarity 34.11
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: CLASSIFICATION:
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STREET: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 VKILMEQDFH-----AERVNEFLREVAIMKRLRHPNIVLFMGAVTQPPNLSIVTEYLSRG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 WEVLSRKOPFEDVTNPLOIMYSVSOGHRPVINEESLPYDIPH--RARMISLIESGWAQNP 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
          Sequence 2, Application PC/TUS9307347
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 376; DB 5; Length 82
Pred. No. 3.2e-27;
); Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07347
FILING DATE: 19930805
                                                                                                                                                                                                             STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPN-1086
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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30.7%; Pre-
tive 60;
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Patent No. 6096539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Miller, Suzanne E. REGISTRATION NUMBER: 32,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 2:
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793 WKRPSFATIMDLLRPLIKS 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 821 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 30.7
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / MOLECULE TYPE: protein
PCT-US93-07347-2
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
PCT-US93-07347-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-329-418-6
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                                                                                                                                                                                                                                                                                                                                                                                                         68 EILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHE 127
                                                                                                                                                                                                                                                                                                                                                                                                                           128 IALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Gaps
                                                                                                                                                                                                                                                                                                                                         13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL---HIHTPLLDSER-KDVLREA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 HRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSFLKCLIELEPV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.0%; Score 369; DB 3; Length 263; Best Local Similarity 32.4%; Pred. No. 2.6e-27; Matches 94; Conservative 56; Mismatches 104; Indels
REGISTRATION NUMBER: 36,677
REFRENCE/DOCKET NUMBER: KIN-2CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650.327-3400
TELEFAX: 650 327-3431
TELEFAX:
                                                                                                 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-035-706-5
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Search completed: June 14, 2001, 08:06:04 Job time: 96 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 14, 2001, 08:04:28 ; Search time 13.68 Seconds (without alignments) 1352.190 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-445-223-1 2829 1 MNGEAICSALPTIPYHKLAD......PEILVVSRSPSLNLLQNKSM 540

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P57078 homo sapien	mus m	arab		P18160 dictyosteli			043318 homo sapien			Q02779 homo sapien	-	caenc	homo	уошо	bos t	P28028 mus musculu		P27966 avian rous-	P51617 homo sapien	homo	•	P34908 coturnix co	P42682 mus musculu	P43404 mus musculu	P24604 mus musculu		_	-	m		681	P08630 drosophila
SUMMARIES	QI	ANR3_HUMAN	RIP_MOUSE	CTR1_ARATH	RIP_HUMAN	KYK1_DICDI	M3K7_MOUSE	KYK2_DICDI	M3K7_HUMAN	ANPB_ANGJA	ANPB_RAT	M3KA_HUMAN	RLK5_ARATH	KRAF_CAEEL	ANPB_HUMAN	M3K9_HUMAN	ANPB_BOVIN	KRAB_MOUSE	RMIL_AVII1	RMIL_AVEVR	IRA1_HUMAN	KRAB_HUMAN	RMIL_CHICK	RMIL_COTJA	TXK_MOUSE	ZA70_MOUSE	TEC_MOUSE	TEC_HUMAN	KRAF_DROME	SPK1_DUGTI	0	SEA_AVIET	TXK_HUMAN	SRC2_DROME
	DB	-	٦	Н	Н	Н	-	-	٦	٦	7	-	Н	Н	Н	~	-	Н	-	-	Н	Н	-	Н	П	-	-	Н	7	Н	-	Н	_	Н
	Query Match Length	832	656	821	671	1584	579	410	909	1050	1047	954	666	813	1047	394	1047	328	367	450	712	765	806	807	527	618	630	631	781	497	619	370	527	290
de	Query Match	19.1	13.9	13.3	13.0	11.1		10.7	10.6		10.3																		9.6				9.4	9.5
	Score	541.5	394	376	369	313.5	311	303.5	300.5	295	292.5	290	289.5	287.5	287.5	284	280.5	277.5	277.5	277.5	277.5	277.5	277.5	277.5	273.5	273	272.5	272.5	272	271.5			265.5	10
	Result No.	1	7	m	4	ល	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P46573 arabidopsis	O24585 zea mays (m	Q62406 mus musculu								P15208 mus musculu	
APKB_ARATH	CRI4_MAIZE	IRA1_MOUSE	7LES_DROME	IG1R_RAT	BTK_MOUSE	EPA3_RAT	TMK1_ARATH	DDR1_MOUSE	EPA5_CHICK	INSR_MOUSE	CLV1_ARATH
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412	901	693	2554	1370	629	984	942	911	1013	1372	980
9.5	9.5	0.6	8.9	8.9	8.9	8.8	8.8	8.7	8.7	8.7	8.7
60.5	259	254	251.5	251	250.5	249	248.5	247.5	247.5	247.5	247
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ALIGNMENTS

us-09-445-223-1.rsp

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Matches 131; Conservative
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InterPro; IPR000488; -.
InterPro; IPR000719; -.
InterPro; IPR002290; -.
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Pfam; PF00069; pkinase;
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DOMAIN
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BINDING
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                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                     84 ICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLL 143
                                                                                                                                                                                                                                                                                                                                                                                        140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SSSE--SKLPSSGSGKRLS-GVS-------SVDSAFSSRGSLSLS 438
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN
                                                                                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                              Gaps
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STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
MEDLINE=95277838; PubMed=7538908;
Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
**IRP: a novel protein containing a death domain that interacts with Fas/APO-1 (CD95) in yeast and causes cell death.";
                                                                                                                                                                                                                                                                               GASGIVSSARHADWRVQVAVK---HLHIHIPLLDSERKDVLREAEILHKARFSYIFPILG
                                                                                                                                                                                                                                                                                                    QKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRAR----MISLIESGWAQNPDERPSF-------LKCLIELEPVLRTFEEITFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: :: | |: | |: | ESEVIIRVTCPLSSPQEITSETEDL/CEKPDDEVKETAHDL/DVKSPPEPRS------E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 GSPETSRSLPAPQ-DNDF-LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 CSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKED
                                                                                                                                                                                                                                                                                                                                                                                                                             HHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG - GTIIYMPPENYEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 YELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL
                                                                                                                                                                                                                                            Indels 113;
                                                                                                                                                                                                           Length 832;
                                                                                           PP (BY SIMILARITY).
PP (BY SIMILARITY).
SIMILARITY.
5D8FFFD5F04F7ECB CRC64;
                                                                                                                                                                                                       19.1%; Score 541.5; DB 1;
31.7%; Pred. No. 2.9e-30;
.1ve 77; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 AA
ANK 6.
ANK 7.
ANK 9.
ANK 10.
ANY (BY
ATP (BY
BY SIM]
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746
780
811
36
51
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                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIP_MOUSE
Q60855;
                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                             NP_BIND
BINDING
 REPEAT
REPEAT
REPEAT
                                                          REPEAT
                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YPQDENDRSVQA------KLQEEASYHAF------GIFAEKQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
1 81:513-523(1995).

FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND FUNITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO THERI IN A THEDEPENDENT PROCESS. REQUIRED FOR THERI ACTIVATION OF NF-KAPPA B. TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHHDLKTQNILLDNEFHVKIADFGLSKWRMMS-LSQSRSSKSAP-----EGGTIIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 NVEEILEYCPREI-----ISLMERCWQAIPEDRPTFLGIEEEFRPFYLSHFEEYV-EED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 LSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDV-LREAEILHKARFSYIFPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIIIEEGNYSLVMEYMEKGNLMHVL--KTQI-DVPLSLKGRIIVEAIEGMCYLHD--KGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 VINE--ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEP-VLRTFEEITFLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 VIQLKK-----TKLQSVSSAIHLC------DKKKMELSLNIPVNHGPQEESCGSSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 394; DB 1; Length 656;
Pred. No. 4e-20;
66; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> I.
ABB350B523879933 CRC64;
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ATP (BY SIMILARITY)
BY SIMILARITY.
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31.0%;
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                                                                                                                                                                                                                                               STRAIN-CV. COLUMNIA, TISSUE-Seedling, MEDLINE-93161417; PubMed-8431946; Kieber J.J., Rothenberg M., Roman G., Feldmann K.A., Ecker J.R.; CTR1, a negative regulator of the ethylene response pathway in Arabidopsis, encodes a member of the raf family of protein kinases.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND ADULT PLANTS.
-!- MISCELLANEOUS: CTR1 MUTANTS DISPLAY ETHYLENE-TREATED PHENOTYPES,
RESULTING IN PLANTS WITH SWALL, UNEXPANDED LEAVES AND WHOSE SEED
COTYLEDON GROWTH IS IMPAIRED.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.-W., Rudd S.
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE
                                                                                                                                   Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D->E: IN CTR1-1; EXHIBITS ETHYLENE-
TREATED PHENOTYPE.
2922D3DCDOCC15BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
E->K: IN CTR1-4; EXHIBITS ETHYLENE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002450;
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS001107; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; AIP-binding.
                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                               821 AA.
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L08790; AAA32780.1; -
EMBL; AL162506; CAB82938.1; -.
HSSP; P11362; lFGI.
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                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000719; -. InterPro; IPR002290; -. Pfam; PF00069; pkinase; PROSITE; PS00107; PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565
                                                                                                                                                                                                                                                                                                                                  Cell 72:427-441(1993).
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N:A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821 AA;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                            CTR1_ARATH
Q05609;
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MUTAGEN
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NP_BIND
BINDING
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CTR1_ARATH
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                                    576
                                                                           101
                                                                                                              631
                                                                                                                                                    161
                                                                                                                                                                                                                                                                     741
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                                                                                                                                                                                                                                                                                                                                  RIP_HUMAN STANDARD; PRT; 671 AA.
013546; 013180;
01-NOV-1997 (Rel. 35, Created)
01-NOV-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SERINE/THREDNINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: INTERÁCTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TUFRI IN A TUFDEPENDENT PROCESS. REQUIRED FOR TUFRI ACTIVATION OF NF-KAPPA B. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95277838; PubMed-7538908; Stanger B., Leder P., Lee T.-H., Kim E., Seed B.; Ranger B.Z., Leder P., Lee T.-H., Kim E., Seed B.; Ras/APO-1 (CD95) in yeast and causes cell death."; Cell 81:513-523(1995).
                                                                                                                                                                                                                                                    --IPYHKLADLRYLSRGASGTVSSARHADWR-VQVA
                                    520 MNAPPISQPVPNRANRELGLDGDDMDIPW---CDLNIKEKIGAGSFGTVHRAEWHGSDVA
                                                                                                 SINELLHRKTE:YPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVK
                                                                                                                                                                       WEVLSRKOPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNP
                                                                         VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG
                                                                                                                                                                                                                              IADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Umbilical vein endothelial cells;
MEDLINE=96200892; PubMed=8612133;
Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
"TNF-dependent recruitment of the protein kinase RIP to the TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huang J., Hsu H., Baichwal V.R., Goeddel D.V.; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor-1 signaling complex.";
Immunity 4:387-396(1996).
                                                                                                                                                                                                                                                                                                                                                                                       278 DERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                           793 WKRPSFATIMDLLRPLIKS 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
MNGEAICSALPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                           46
                                                                                                                                                    102
                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                           220
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EMBL; U50062; AAC32232.1; -.

12;

Gaps

50;

13.3%; Score 376; DB 1; Length 821; 30.7%; Pred. No. 9.6e-19; Live 60; Mismatches 111; Indels

Conservative

Query Match Best Local Similarity Matches 98; Conserv

us-09-445-223-1.rsp

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RRARRENT RARRENT RRARRENT RRARRENT RRARRENT RRARRENT RRARRENT RRARRENT RRAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE------GGTIIYMP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INE--ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 VDDITEYCPREI-----ISLMKLCWEANPEARPTFPGIEEKFRPFYLSQLEESVEEDVK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLKK-----TKLQSV-----SSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 SLKKEYSNENAVVKRMOSLQLDCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
PROTEIN KINASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILHKARFSYIFPIL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDSGGFGKVSLCFH---RTQGLMIMKTVYKGPNCIEHNEALLEEAKMMNRLRHSRVVKLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.0%; Score 369; DB 1; Length 671;
Llarity 28.8%; Pred. No. 2.2e-18;
Conservative 67; Mismatches 146; Indels
                                                                                                                                                                                                                                  PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50017; DEMU-DOMAIN; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> S (IN REF. 3).
BADC4E7E70456ABE CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ARG.
T -> S (IN REF.
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BY SIMILARITY.
DEATH DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 LHENSGSPETSRSLPAPQDNDFLSRKAQD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEH-----PQEENEPSLQSKLQD 380
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MEDLINE-97053827; PubMed-8898241;
                                                                                                                                                                                                                                                                                                                                                                                                                      ATP
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Σ
                                                                             InterPro: IPR000488; -.
InterPro: IPR000719; -.
InterPro: IPR002290; -.
Pfam; PF00531; death; 1.
Pfam; PF00699; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75958
   U25994; AAC50137.1;
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                               P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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SEQUENCE FROM N.A.
                                                              MIM; 603453;
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ID KYKI_DICDI
AC P18160;
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Matches 112;
                                                                                                                                                                                                                                                                                                                                                              Apoptosis.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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DR R DDR KWW KWW KWW KWW SDR KWW KWW SDR KWW SDR KWW SDR KWW KWW SDR KWW KWW KWW KWW KWW SDR KWW KWW KWW SDR KW SDR KW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH A PEAK DURING THE MOUND STAGE OF MORPHOGENESIS.
-i- SIMILARITY: TO OTHER PROTEIN "TROSINE KINASES BUT ALSO TO SERINE/THREONINE PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLREAEILH 71
Nuckolls G.H., Osherov N., Loomis W.F., Spudich J.A.; "The Dictyostelium dual-specificity kinase splA is essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 313.5; DB 1; Length 1584; 28.1%; Pred. No. 5.3e-14; cive 59; Mismatches 119; Indels 55;
                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
D -> R (IN REF. 2).
V -> L (IN REF. 2).
WW; 5D1589458D8E01E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY - ASN.
POLY - ASN.
POLY - ASN.
POLY - ASN.
POLY - PHE.
POLY - SER.
POLY - SER.
POLY - GEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY - PRO
                                                    Development 122:3295-3305(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32174; AAB41125.1; -. EMBL; M33785; AAA33202.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.1 ses 91; Conservative
                                         spore differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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NP_BIND
BINDING
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Matches
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10;

64227 MW; 97C8F6F3C8E283EE CRC64;

579 AA;

SEQUENCE

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                                1341 KLRHPNVVQFLGACTAGGEDHHCIVTEWMGGGSLRQFLTDHFNLLEQNPHIRLKLALDIA 1400
                                                                                                      1455
                                                                                                                                                        130 LGVNYLHNMTPPLLHHDLKTQNILLDN------EFHVKIADFGLSKWRMMSLS 176
                                                                                                                                    QSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPL 236
                                                                                                                                                                                                      QIMY-SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
72 KARFSYIFPILGICNE--PEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIANE-96123277; PubMed-8533096;
MEDIANE-96123277; PubMed-8533096;
Yamaguchi K., Shirakabe K., Shibuya H., Irie K., Ohishi I., Ueno N., Taniguchi T., Nishida E., Matsumoto K.;
"Identification of a member of the MAPKKK family as a potential mediator of TGF-beta signal transduction.";
Science 270:2008-2011(1995).
-I- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKKS.
MEDIATOR.OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B
                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C210RF7.
                                                                                                                                                                                                                          01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
MITGGEN-ACTIVATED PROTEIN KINASE KINASE 7 (EC 2.7.1.-)
(TRANSFORMING GROWTH FACTOR-BETA-ACTIVATED KINASE 1) (TGF-BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase, Serine/threonine-protein kinase, ATP-binding. DOMAIN 8 16 POLY-SER.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                             579 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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----TFKQIIVHLKEMEDQGVSS 1569
                                                                                                                                                                                                                                                                         296 TFEEITFLEAVIQLKKTKLQSVSS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D76446; BAA11184.1; -.
MGD; MGI:1346877; Map3k7.
InterPro; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, (Rel. 40,
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63
156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATED KINASE 1).
MAP3K7 OR TAK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                           M3K7_MOUSE
Q62073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
BINDING
ACT_SITE
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M3K7_MOUSE
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                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                 83 RVNHPNIVKLYGACLNP--VCLVMEYAEGGSLYNVLHGAEPLPYYTAAHAMSWCL---- 135
                                                                                                                                                                                                                                                                                                                                                                       243 SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTF----E 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 PLOYPCOYSDEGOSNSATSTGSFMDIASTNTSNKSDTNMEGVPATNDTIKRLESKLLKNQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 QDLTVTGTEPGQVSSRSSSPSVRMITTSGPTSEKPARSHPWTPDDSTDTNGSDNSIPMAY 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 KARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYP-----DVAWPLRFRIL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AKQQSESGRLSLGASRGS--SVESLPPTSEGKRMSADMSEIE-ARIVATAGNGQPRRRSI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 WDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTE 453
                                                                       13 IPYHKLADLRYLSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILH 71
                                                                                                          31 IDYKEIEVEEVVGRGAFGVVCKAK---WRAKDVAIKQIE----SESERKAFIVELRQLS 82
                                                                                                                                                                                                                                                                                                                       126 HEIALGVNYLHNMTP-PLLHHDLKTQNILL-DNEFHVKIADFGLSKWRMMSLSQSRSSKS
                                                                                                                                                                                                                                             244 HNGTRPPL-IKNLPKPIE-----SLMTRCWSKDPSQRPSMEEIVKIMTHLMRYFPGADE
                                                                                                                                                                                                                                                                                                                                                                                                                                            299 EI------TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 ACLNQSLD------ALESRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEF
                                                                                                                                                                                                                                                                                             184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNP-LQIMYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 GPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHS----
                                      100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90287147; PubMed=1972546;
Tan J.L., Spudich J.A.;
"Developmentally regulated protein-tyrosine kinase genes in
 Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum.";
Mol. Cell. Biol. 10:3578-3583(1990).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES SERINE/THREONINE PROTEIN KINASES.
                                    97; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538
 DB 1;
11.0%; Score 311; DB 1
23.5%; Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 VAELDQDEKDQQNTSRLVQEHKKLLDENKSLSTYYQQCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 AKVIVQKLKD--NKQMGLQPYPEILVVSRSPSLNLLQNK
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                                      Conservative
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                   Similarity
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P18161;
                                    Matches 136;
Query Match
Best Local S
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        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 YIFPILGICNEPEFLGIVTEYMPNGSLNELLHR-----KTEYPDVAWPLRFRILHEIAL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 I---YMPPENYEPGOKSRASIKHDIYSYAVITWEVLSRKQPFEDV---TNPLQIMYSVSQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 CNPRWRPPELTK--NLGHYSEKVDVYCFSLVVWEILTGEIPFSDLDGSQRSAQVAYA--- 325
                                                                                                                                                                                                                                                                                                                                                                 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           DLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE--RKDVLREAEILHKARFS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an
                                                                                                                                                                  Pfan: PF00069; pkinase; 1.
PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakurai H., Shigemori N., Hasegawa K., Sugita T.;
"TGF-beta-activated kinase I stimulates NF-kappa B activation by
NF-kappa B-inducing kinase-independent mechanism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M3K7_HUMAN STANDARD; PRT; 606 AA.
043317; 043319;
01-0CT-2000 (Rel. 40, Crasted)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
MITOGEN-ACTIVATED PROTEIN KINASE KINASE 7 (EC 2.7.1.-)
MITOGEN-ACTIVATED PROTEIN KINASE XINASE 7 (EC 2.7.1.-)
ACTIVATED KINASE 1).
                                                                                                                                                                                                                                                                                                                                         Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 GHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 GLRPPIPEYCDP-----ELKILLTOCWEADPNDRPPFTYIVNKIKEI 367
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and the
                                                                                                                                                                                                                                                                                                   E93918B605B9AEC1 CRC64;
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                        10.7%; Score 303.5; DB 1; llarity 30.1%; Pred. No. 4.2e-14; Conservative 57; Mismatches 102;
the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                               or send an email to license@isb-sib.ch).
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M
                                                                                        EMBL; M33784; AAA33203.1; -.
                                                                                                                                                                                                                                                                                                    46386
                                                                                                                  HSSP; P11362; 1FGI.
DictyDb; DD03011; pykB.
InterPro; IPR000719; -.
InterPro; IPR001245; -.
                                                                                                    PIR; B35670; B35670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                             114
135
232
410 AA;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTF----E 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNH 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 KARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYP-----DVAWPLRFRIL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 HEIALGVNYLHNMTP-PLLHHDLKTQNILL-DNEFHVKIADFGLSKWRMMSLSQSRSSKS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 AKQQSESGRLSLGASRGS--SVESLPPTSEGKRMSADMSEIEARIAATTAYSKPKRGHRK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 IPYHKLADLRYLSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILH 71
them. Biophys. Res. Commun. 243:545-549(1998). FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKKS. MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : : : : 1 : 1 : 297 PLQYPCQYSDEGQSNSATSTGSFMDIASTNTSNKSDTNMEQVPATNDTIKRLESKLLKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION.
-:- ALTENATIVE PRODUCTS: 3 ISOFORMS; 1A, 1B (SHOWN HERE) AND 1C;
PRODUCED BY ALTENATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE KIDRASE JOBFAMILY.
-:- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C21ORF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNP-LQIMYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 606;
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PROSITE; PS00108; PROTEIN_KINASE_AT; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NI)
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MISSING (IN ISOFORM 1A).
PLAAPCPONSE -> ARTSCRIEGG (I
MISSING (IN ISOFORM IC).
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ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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22.8%; Pred. No. 1.2e
:ive 96; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB009357; BAA25026.1; -. EMBL; AB009356; BAA25025.1; -. EMBL; AB009358; BAA25027.2; -.
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Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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DOMAIN

B 14

DOMAIN

36

291

NP_BIND

BINDING

63

63

ACT_SITE

156

VARSPLIC

VARSPLIC

519

606
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156
404
509
519
606 AA;
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VARSPLIC
SEQUENCE
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[1]
SEQUENCE FROM N.A.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PECCETORSOR (ANP-B) (ANPRB) (GC-B)
(GUANYLATE CYCLASE) (EC 4.6.1.2) (NPR-B) (ATRIAL NATRIURETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANBOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLEY RESPONSIBLE FOR THE CLEARANGE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC
                                                                                                                      SERLQPGIAQQWIQSKREDIVNQMTEACLNQSLD------ALLSRDLIMKEDYE 475
                                                                                                                                                                                                                                                                                         535. KVQT-----EIALLLQ----RKQELVAELDQDEKDQONTSRLVQEHKKLLDENKSLSTY 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anguilla japonica (Japanese eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguilloidei;
Anguillidae, Anguilla.
380 -CYFMKLHHCP----GNHS-----WDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGN 427
                                                         415 TASFGNILDVPEIVISGNGQPRRRSIQDLTVTGTEPGQVSSRSSSPSVRMITTSGPTSEK 474
                                                                                                                                                                   475 PTRSHPWTPDDSTDTNGSDNSIPWAYLTLDHQLQPLAPCPNSKESMAVFEQHCKMAQEYM 534
                                                                                                                                                                                                                                         LVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKD--NKQMGLQPYPEILVVSRSPSLN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirose S.; "Cloning and expression of eel natriuretic peptide receptor B and \ensuremath{\text{and}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katafuchi T., Takashima A., Kashiwagi M., Hagiwara H., Takei Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1050 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94298823; PubMed=7913035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D25417; BAA05007.1; -. HSSP; Q02846; 1AWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7937
                                                                                                                                                                                                                                                                                                                                                                534 LLQNK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                585 YQQCK 589
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ID ANPB_ANGJA
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation BRECURSOR (ANP-B) (ANPRB) (GC-F (GUANYLATE CYCLASE) (EC 4.6.1.2) (NPR-B) (ATRIAL NATRIURETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 YHKLADLRYL--SRGAS-GTVSSARHADWRV------QVAVKHLHIHTPLLDSERK 61
                                                                                                                                                                                                                                       æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625 YSLINDIVKGMNFLHNSYIG-SHGNLKSSNCVVDSRFVLKITDYGLASFRSSCENEDSHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 YHKCAGSRLTISQRGSSYGSLITA-HGKYQLFAKTGYFKGNLVAIK--HVNKKRIELTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 FRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684 LYAKKLWTAPE--LLIYDRHPPQGTQKG------DVYSFGIILQEIALRNGPFYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SRSSKSAPEGGTIIY--MPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                    ATRIAL NATRIURETIC PEPTIDE RECEPTOR EXTRACELLULAR (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                Transmembrane; Glycoprotein; Phosphorylation; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F3AC6DDD17BD3832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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INTERCHAIN (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 295; DB 1; 29.0%; Pred. No. 5.9e-13;
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            Pfam; PF01034; ANF_receptor; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00255; NATREPTIDER.
PROSITE; PS00425; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Mismatches
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Best Local Similarity 29.09
Matches 87; Conservative
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                                                                                                                                                                                                                                                           460
481
1050
790
                                                                                                                                                                Receptor; Transmembran cGMP synthesis; Signal
rbr001828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 35
366 36
415 41
1050 AA;
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DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR 121

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                                                                                                         -1- SIMILARITY: TO ANP-A ON THE COMPLETE SEQUENCE, AND TO ANP-C IN TH
                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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                    Schulz S., Singh S., Bellet R.A., Singh G., Tubb D.J., Chin H., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
RECEPTOR; Transmembrane; Glycoprotein; Phosphorylation; Lyase; GGMP synthesis; Signal.
                                                                      cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5062C49228CC14A3 CRC64;
                                                                 "The primary structure of a plasma membrane guanylate odemonstrates diversity within this new receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR AND TRANSMEMBRANE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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MEDLINE-89376566; PubMed-2570641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01094; ANF_receptor; 1. Pfam; PF00069; pkinase; 1. PRINTS; PR00255; NATPEPTIDER.
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InterPro; IPR000719; -.
InterPro; IPR001054; -.
InterPro; IPR001170; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001828; -.
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1047 AA;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                   777 PDF----GQIKGFIRRFNKEGGTSILDNLLLRAMEQYANNLEKLVEERTQAYLEEKRKAEA 832
                                                         181
                                                                                                                                              182 KSAPEGGTIIY-----MPPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPF--E 230
                                                                                                                                                                                                                                                                                                                     281 PSFLKCLIELEPVLRTFEE---ITFLE-AVIQLKK-----TKLQSVSSAIHLCDKKKMEL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dorow D.S., Devereux L., Dietzsch E., de Kretser T.; "Identification of a new family of human epithelial protein kinases
|| | : : :| : : : | | 564 -VLFELKHMRDVQFNHLTTRFIGACIDPPNICIVTEYCPRGSLQDIL--ENDSINLDWMFR
                                                                                  621 YSLINDLVKGMAFLHNSIIS-SHGSLKSSNCVVDSRFVLKITDYGLASFR-----S
                                                                                                                                                                         728 GLDLSPKEIVQKVRNGQRPYFRPSIDRTQLNEE------LVLLMERCWAQDPTER
                                                           122 FRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSS
                                                                                                                                                                                                                                   DV-TNPLQIMYSVSQGHRPV-----INEESLPYDIPHRARMISLIESGWAQNPDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eur. J. Blochem. 213:701-710(1993).
-!- TISSUE SPECIFICITY: EXPRESED IN BRAIN AND SKELETAL MUSCLE.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 2.7.1.-)
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BOLOWE-96128179; PubMed-8536694;

BOLOW D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
Sutherland G.R., Simpson R.J.;
"Complete nucleotide sequence, expression, and chromosomal localisation of human mixed-lineage kinase 2.";

Eur. J. Blochem. 234:492-500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katoh M., Hirai M., Sugimura T., Terada M.;
"Cloning and characterization of MST, a novel (putative)
serine/threonine kinase with SH3 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M3KA_HUMAN STANDARD; PRT; 954 AA.
01-2779; 012761; 014871;
01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
MITOGEN-ACTIVATED PROTEIN KINASE KINASE ID (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST).
MAP3KIO OR MLK2 OR MST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95249256; PubMed=7731697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Colon epithelium;
MEDLINE=93238756; Pubmed=8477742;
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                                                                                                                                                                                                                                                                                                                                                                                                            332 SLNIPVNHGPQEE 344
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21;

Indels 77; Gaps

Length 1047;

YHKLADLRY-LS-RGAS-GTVSSARHADWRV------QVAVKHLHIHTPLLDSERK 61

10.3%; Score 292.5; DB 1; 1larity 27.3%; Pred. No. 8.8e-13; Conservative 80; Mismatches 114;

Similarity

Query Match Best Local Simi Matches 102;

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RLK5_ARATH
P47735;
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                                                                                                                                                                                                          Serine/threonine-protein kinase; Tyrosine-protein kinase;
SH3 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSER-----KDVLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSQSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 NPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPV
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                                                                                                                                                                                                                                                                                                                                                                                                   10.3%; Score 290; DB 1; Length 954; 23.7%; Pred. No. 1.2e-12; tive 78; Mismatches 174; Indels 144;
                                                                                                                                                                                                                                                                                     LEUCINE-ZIPPER (BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
ARG/LYS-RICH (BASIC).
SRL -> AV (IN REF. 2).
G -> S (IN REF. 2).
G -> R (IN REF. 2).
V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                        538F4AAA559B0ABA CRC64;
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ATP (BY SIMILAR
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or send an email to license@isb-sib.ch).
                                                                                                                                 Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR001217; PRICHEXTENSN.
PRINTS; PR001217; PRICHEXTENSN.
PROSITE; PS00100; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001018; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_ST; 1.
                                   EMBL; X90846; CAA62351.1; --
EMBL; Z44615; CAA88531.1; --
PIR; S32468; S32468.
HSP; P00523; 2PTK.
MIM; 600137; --
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                                                                                                                                                                                                                        domain.
                                                                                                       IPR001452; -.
                                                                                   InterPro; IPR000719; -. InterPro; IPR001245; -.
                                                                                                                       Pfam; PF00018; SH3; 1.
Pfam; PF00069; pkinase
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Matches 123;
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                                                                                                                                                                                                                            Horn M.A., Walker J.C.;
"Blochemical properties of the autophosphorylation of RLK5, a receptor-like protein kinase from Arabidopsis thaliana.";
Blochim. Blophys. Acta 1208:65-74(1994).
-i- COFACTOR: HAVE SIGNIFICANTLY GREATER ACTIVITY IN THE PRESENCE OF MN2+ THAN MG2+.
Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaugnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hammed A., Lodhi M., Johnson A., Chen E., Marra M., Martienssen R., McCombie W.R.; Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: EXPRESSED IN ROOTS AND ROSETTES.
-!- PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
-!- SIMILARITY: TO PROTEIN KINASES IN THE C-TERMINUS. BUT DOES NOT SEEM TO HAVE CONSERVED A KINASE ACTIVITY.
-!- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).
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Prono605, LRR; 14.

Prims, Pro0069; Prinse; 1.

PROSITE; PS00107; PROTEIN.KINASE_ATP; 1.

PROSITE; PS001019; PROTEIN.KINASE_ATP; 1.

PROSITE; PS001019; PROTEIN.KINASE_DOW; 1.

PROSITE; PS50011; PROTEIN.KINASE_DOW; 1.

Transferase; Serine/Threonine-protein kinase; ATP-binding;

Transmembrane; Glycoprotein; Phosphorylation; Leucine-rich repeat;
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MEDLINE-94368830; PubMed-8086440;
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EMBL; AL161572; CAB79651.1;
HSSP; P00523; 2PTK.
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                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLH--RKTEYPDVAWPLRF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RILHEIALGVNYL-HNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      16 HKLADL----RYLSRGASGTVSSARHADWRVQVAVKHLHIHTP-----LLDSERKDVL- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: PROTEIN LINEAR THAT PARTICIPATES IN THE INDUCTION OF C.ELEGANS VULVA. ACTS DOWNSTREAM OF THE RAS PROTEIN LET-60.
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
-i- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 KSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 VSQ-----GHRPVINEESLPYDIPHRARMISLIESG---WAQNPDERPSFLKCLIELEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-93247635; PubMed-8483497;
MEDLINE-93247635; PubMed-8483497;
Han M., Golden A., Han Y., Sternberg P.W.;
"C. elegans lin-45 raf gene participates in let-60 ras-stimulated vulval differentiation.";
Nature 363:133-140(1993).
                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       31;
    (POTENTIAL)
                                                                                                                                                                                                                                   K->E: LOSS OF CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                           DB 1; Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
RAF HOMOLOG SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                         F5793D899EA0C6A7 CRC64;
N-LINKED (GLCNAC...
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                       Mismatches 123;
                                                                                                                                                                                                                                                                                                                           10.2%; Score 289.5; DB 1 32.3%; Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               813
                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                         109095 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last seq
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                         999 AA;
                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
    150
185
210
269
282
452
689
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Best Local Simi
Matches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRAF_CAEEL
Q07292;
                                                                                                                                                               NP_BIND
BINDING
ACT_SITE
MUTAGEN
SEQUENCE
                          CARBOHYD
CARBOHYD
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PIR; S05514; S05514.
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EMBL;
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   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANPE-HUMAN STANDARD; PRT: 1047 AA.
P20594; Q9UQ50; 060871;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANTLATE CYCLASE) (EC 4.6.1.2) (NPR-B) (ATRIAL NATRIURETIC PEPTIDE B-TYPE RECORD).
NPR2 OR ANDRB.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                    | :| | | : : | | | : : | 579 | S23 KNEVAVLKKTRHLNVLLFMGWVREPE-IAIITQWCEGSSLYRHIH--VQEPRVEFEMGAI 579
                                                                                                                                                                                                                                                                                                                                                                                    QSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPL 236
                                                                                                                                                                                                                                                                                                                                                                                                 466 POKPHHE--DWEILPNEFIIOYKVGSGSFGTVYRGEFFGTVAIKKLNVVDP-TPSQMAAF 522
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                    PTIPYHKLADLRYLS-----RGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang M.S., Lowe D.G., Lewis M., Hellmiss R., Chen E., Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                          64 LREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR--
                                                                                                                                                                                                                                                                                                                                               122 FRILHEIALGVNYLHNMTPPLLHHDLKTQNI-LLDNEFHVKIADFGL----SKWRMMSLS
                                                                                                                                                                                                                                                                                                                                                                                                                           237 QIMYSVSQGH-RPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                   Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                DB 1; Length 813;
                                                                                                                                                     PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                          BY SIMILARITY.
6376E968C6859E49 CRC64;
                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                              Score 287.5; DB 1;
Pred. No. 1.4e-12;
65; Mismatches 127;
                                                                          Pfam; PF00069; pkinase; 1.
PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GEVLERLRDIILPKLTRSQSAPNVLHL 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 TFEEITFLEAVIQLKKTKLQSVSSAIHL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE-89365195; PubMed=2570358;
                         HSSP, P11362; 1AGW.
InterPro; 1PR000719; -
InterPro; IPR002219; -
InterPro; IPR002290; -
Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                                    90491 MW;
                                                                                                                                                                                                                             10.28;
27.78;
         AAA28142.1;
                                                                                                                                                                                                                                                91; Conservative
                                                                                                                                            binding.
                   S33261; S33261
                                                                                                                                                                                                   813 AA;
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
          L15347;
                                                                                                                                            Phorbol-ester
                                                                                                                                                                                         ACT_SITE
SEQUENCE
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                       NP_BIND
BINDING
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                   177
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                                                                                                                                                                                                                                                       Rehemudula D., Nakayama T., Soma M., Takahashi Y., Uwabo J., Sato M., Izumi Y., Kanmatsuse K., Ozawa Y.; Stroture of the type B human natriuretic peptide receptor gene and association of a novel microsatellite polymorphism with essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
       oţ
"Differential activation by atrial and brain natriuretic peptides two different receptor guanylate cyclases.";
Nature 341:68-72(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mollerup S.,
Schlatter E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney;
Hirsch J.R., Meyer M., Magert H.J., Forssmann W.G., Mollerup
Herter P., Weber G., Cermak R., Ankorina-Stark I., Schlatter
Kruhoffer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (SHORT ISOFORM).
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                                                                                                                                                SEQUENCE FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Circ. Res. 84:605-610(1999).
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BAA81737.1;
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                                                                                                                                                                                                                     PubMed=10082481;
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LL -> KADSHSSPSLHLSQTLPTCFFSKGQSVLGLLA
(IN SHORT ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 KSAPEGGTIIY-----MPPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPF--E 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 PDF----GOIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEERTQAYLEEKRKAEA 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 -VLFELKHMRDVQFNHLTRFIGACIDPPNICIVTEYCPRGSLQDIL--ENDSINLDWMFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 YSLINDLVKGMAFLHNSIIS-SHGSLKSSNCVVDSRFVLKITDYGLASFR-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728 GLDLSPKEIVQKVRNGQRPYFRPSIDRTQLNEE-----LVLLMERCWAQDPAER
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                           ATRIAL NATRIURETIC PEPTIDE RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                              PRINTS; PRO0255; NATEEPIDER.
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS500115; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase; CGMP synthesis; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1047;
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817FB74D6B31F7EF CRC64;
                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.2%; Score 287.5; DB 1;
Best Local Similarity 27.1%; Pred. No. 2e-12;
Matches 101; Conservative 80; Mismatches 115;
                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                     InterPro; IPR001828; -. Pfam; PF01094; ANF_receptor; 1. Pfam; PF00069; pkinase; 1.
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1047 AA; 117021
                            InterPro; IPR000719; -. InterPro; IPR001054; -.
                                                           InterPro; IPR001170; -.
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833 LLYQILPHSVAEQ 845
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TRANSMEM
DOMAIN
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 QVAVKHLHIHTPLLDSER--KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPN 100
                                                                                                                   01-OCT-2000 (Rel. 40, Last annotation update)
MITGGEN-ACTIVATED PROTEIN KINASE KINASE 9 (EC 2.7.1.-) (MIXED
LINEAGE NATURASE 1) (FRAGMENT).
MAP3K9 OR MIKI OR PRKEI.
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26 EVAVKAAR-HDPDEDISQTIENVRQEAKLFAMLKHPNITALRGVCLKEPNLCLVMEFARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 IKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMIS
                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%; Score 284; DB 1; Length 394; 26.4%; Pred. No. 9.1e-13; ive 62; Mismatches 125; Indels 122;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
LEUCINE-ZIPPER (BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
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DBE40B7D31047FD8 CRC64;
                          394 AA
                                                                                                 Last sequence update)
                          PRT;
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                                                                                                                                                                                                                                                                                                                                                           TISSUE-Colon epithelium;
MEDLINE-93238756; PubMed-8477742;
                                                                      28, Created)
28, Last seg
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                          STANDARD;
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                                                                  01-FEB-1994 (Rel. 01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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354
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                      M3K9_HUMAN
P80192;
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DOMAIN
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BINDING
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A3K9_HIMAN
A3K9_HIMAN
A3K9_HIMAN
A3K9_HIMAN
A101-0FEB
DT 01-0FEB
DT 01-0FEB
DT 01-0FEB
DE LINEAG
GN MAMP3K9
OS HOMO SO
OC MAMMAN
OX NCBL_TI
RR TIGENT
RA DOLOW
RT "Ident
RA DOLOW
RT "Ident
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RY "Inter
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DR PROSI
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Search completed: June 14, 2001, 08:04:51 Job time: 23 sec

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OM protein - protein search, using sw model

June 14, 2001, 08:04:28; Search time 53.04 Seconds Run on:

(without alignments)
699.668 Million cell updates/sec

US-09-445-223-1 2829

score:

1 MNGEAICSALPTIPYHKLAD.....PEILVVSRSPSLNLLQNKSM 540 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

198801 seqs, 68722935 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_67:* Database :

piri:* pir2:* pir3;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ď			SUMMARIES	
Result	Score	Query Match	Length	DB	dī	Description
-	394	13.9	656	: ~	I49299	recentor interacti
7	385.5	13.6	829	7	T07406	
æ	376	13.3	821	7	T48400	serine/threonine-p
4	369	13.0	671	7	T09479	serine/threonine p
S	359.5	12.7	963	~	T09911	probable serine/th
φ	359	12.7	1015	7	T00726	
7	348.5	12.3	370	7	T46150	protein kinase ATN
ω	340	12.0	982	~	T06576	probable protein k
σ	'n	11.9	736	~	T05137	protein kinase hom
10	327.5	11.6	406	7	T52626	probable mitogen-a
11	317.5	11.2	462	7	S29851	protein kinase 6 (
12	316.5	11.2	176	7	T02584	hypothetical prote
13	313.5	11.1	1584	7	T18276	protein-tyrosine k
14	312	11.0	579	7	JC5955	transforming growt
15	307	10.9	553	~	T04683	hypothetical prote
16	306.5	10.8	475	7	T12955	probable protein k
17	306.5	10.8	267	7	JC5957	transforming growt
18	306.5	10.8	888	7	A55318	serine/threonine p
19	306.5	10.8	888	7	JC5399	dual leucine zippe
20	305	10.8	784	7	T45697	hypothetical prote
21	303.5	10.7	410	7	B35670	protein-tyrosine k
. 55	302.5	10.7	390	~	T01451	protein kinase hom
23	301.5	10.7	988	~	T48544	MAP3K delta-1 prot
24	300.5	10.6	909	7	JC5956	0
25	300	10.6	443	7	T01182	hypothetical prote
56	297.5	10.5	545	~	T05675	
27	295	10.4	1050	~	S45636	natriuretic-peptid
28	292.5	10.3	668	7	JC2363	protein kinase (EC
29	292.5	10.3	1047	-	OYRTBR	atrial natriuretic

30	292	10.3	1338	7	T18287	protein-tyrosine k
31	290.5	10.3	816	7	T45684	hypothetical prote
32	290	10.3	954	Н	S68178	mixed-lineage prot
33	289.5	10.2	666	_	S27756	receptor-like prot
34	289.5	10.2	1192	7	T48499	receptor-like prot
35	289	10.2	855	7	T10665	hypothetical prote
36	288.5	10.2	871	7	T45692	receptor-like prot
37	288	10.2	884	7	T02731	serine/threonine-s
38	287.5	10.2	813	Н	S33261 ·	protein kinase lin
39	287.5	10.2	1047	٦	OYHUBR	natriuretic peptid
40	287	10.1	929	7	T10664	serine/threonine-s
41	286	10.1	819	7	T45690	receptor-like prot
42	285.5	10:1	694	7	T01134	hypothetical prote
43	284	10.0	394	7	300229	mixed-lineage prot
44	283	10.0	356	7	T50811	ser/thr specific p
4.5	283	10.0	402	7	T51791 ·	ser/thr specific p
ν.					ALIGNMENTS	
RESULT 149299	п					

C; Accession: 144299
R; Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
R; Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
R; Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
R; Status: 513-523, 1995
A; Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
A; Reference number: A56913; MUID:95277838
A; Accession: 146299
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-656 < RES>
A; Cross-references: EMBL:U25995; NID:9829618; PIDN:AAB60487.1; PID:9829619
C; Genetics:
A; Gene: RIP
C; Superfamily: protein kinase homology
F; 15-293/Domain: protein kinase homology < KIN> C;Species: Mus musculus (house mouse) C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999 receptor interacting protein RIP - mouse

19; 24 LSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDV-LREAEILHKARFSYIFPIL 82 82; 13.9%; Score 394; DB 2; Length 656; 31.0%; Pred. No. 1.1e-15; 66; Mismatches 144; Indels Best Local Similarity 31.0% Matches 131; Conservative Query Match δ

83 GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL 142 23 LDSGGFGKVSLCYHRSHGFVILKK---VYTGPNRAEYNEVLLEEGKMMHRLRHSRVVKLL 79 δ

143 LHHDLKTQNILLDNEFHVKIADFGLSKWRMMS-LSQSRSSKSAP-----EGGTIIYM 193 q ò

194 PPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRP 248 g Op ò

249 VINE -- ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEP-VLRTFEEITFLEA 305 249 NVEELLEYCPREJ-----ISLMERCWQAIPEDRPTFLGIEBEFRPFYLSHFEETV-EED 301 g ă

306 VIQLKK-----TKLQSVSSAIHLC------DKKKMELSLNIPVNHGPQEESCGSSQ 350 302 VASLKKEYPDQSPVLQRMFSLQHDCVPLPPSRSNSEQPGSLHSSQGLQMGPVEESWFSS- 360 g ò

351 LHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHK 410 361 -----SPE-----YPQDENDRSVQA-----KLQEEASYHAF------GIFAEKQ 393 qq Qγ

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A Accession: A45178
A Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Rolecule type: DNA
A; Rolecule sequence extracted from NCBI backbone (NCBIP:124878)
A; Note: sequence extracted from NCBI backbone (NCBIP:124878)
C; Genetics:
A; Map position: 5
A; Map position: 5
A; Note: F17C15.150
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C; Keywords: ATP
F; 549-812/Domain: protein kinase homology <KIN>
F; 557-565/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Klm, E.; Seed, B.
Cell 81, 513-523, 1995
A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
A;Reference number: A56913; MUID:95277838
A;Reference number: 138992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 300-513,'S',515-671 <RES>
A;Cross-references: EMBL:UZ5994; NID:g829616; PIDN:AAC50137.1; PID:g829617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520 MNAPPISQPVPNRANRELGLDGDDMDIPW---CDLNIKEKIGAGSFGTVHRAEWHGSDVA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 WEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNP 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IPYHKLADLRYLSRGASGTVSSARHADWR-VQVA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 IADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 376; DB 2; Length 82: 30.7%; Pred. No. 1.6e-14; tive 60; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-671 < HUDA.
A;Cross-references: EMBL:U50062; NID:g3426026; PID:g3426027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine/threonine protein kinase (EC 2.7.1.-) RIP - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T09479; I38992
R;Huang, J.; Hsu, H.; Baichwal, V.R.; Goeddel, E
submitted to the EMBL Data Library, August 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: ATP binding; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 DERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     793 WKRPSFATIMDLLRPLIKS 811
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.77
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z16685
A; Accession: T09479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-829 «WANA
A; Cross-references: EMBL:Y13273; NID:e1050452; PIDN:CAA73722.1; PID:e334294
A; Experimental source: strain UC82B; sub_species Mill
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Υ.
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 10-ppr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Nov-2000
C; Accession: T48400; A45178
R; Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, March 2000
A; Reference number: 224492
A; Accession: T48400
A; Status: preliminary
A; Wolecule Cype: DNA
A; Residues: 1-821 < ABEV>
A; Cross-references: EMBL:AL162506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: cultivar Columbia; BAC clone F17C15
R;Kleber, J.J.; Rothenberg, M.; Roman, G.; Feldmann, K.A.; Ecker, J.R.
Cell 72, 427-441, 1993
A;Title: CTR1, a negative regulator of the ethylene response pathway in Arabidopsis, A;Reference number: A45178; MUID:93161417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                        C;Species: Lycopersicon esculentum (tomato)
C;Date: 14.May-1999 #sequence_revision 14.May-1999 #text_change 08-Oct-1999
C;Accession: T07406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 KOPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQDFHAERL----KEFLREVAIMKRLRHPNIVLFMGAVIQPPNLSIVTEYLSRGSLYRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRFKANTFLSSKTAAGTPE----WMAPEVIRDEPSNE----KSDVYSFGVILWELATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine/threonine-protein kinase ctrl - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 385.5; DB 2;
Pred. No. 4.7e-15;
56; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, May 1997
A;Reference number: 216016
A;Accession: T07406
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%;
33.2%;
                                                                                                                                                                                                          - tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 33.2%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 STIMDMLRPHLKS 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 LKCLIELEPVLRT 296
                                                                                                                                                                                                       probable protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GEAICSALPT--
           411 TTP 413
                                                             394 TKP 396
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Best Local 3
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us-09-445-223-1.rpr

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protein kinase ATN1-like protein - Arabidopsis thaliana
N;Alternate names: protein T3A5.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
C;Accession: T46150; T08394
F;Blococker, H., Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, F.; S submitted to the Protein Sequence Database, December 1999
                                                                                                                                                                                                                                                                                                                                                                                             Submitted to the EMBL Data Library, April 1998
A; Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A; Reference number: 214200
A; Reference number: 214200
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1015 <SHI>A; CESSION A; MOLECULE A; MOLECULE A; CESSION A; MOLECULE A; CESSION A; MOLECULE A; CESSION A; MOLECULE A; CESSION A; CESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Experimental source: cultivar Columbia; BAC clone T3A5
R;Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
A: Introns: 71/3; 219/3; 360/3; 395/2; 760/1; 773/3; 796/3; 830/2; 856/3; 889/3; 912/3
C; Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                         probable serine/threonine-specific protein kinase (EC 2.7.1.-) F22013.21 - Arabidopsi C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T00726
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH, 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE-----RKDVLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1015;
                                QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%; Score 359; DB 2;
llarity 32.9%; Pred. No. 2.1e-13;
Conservative 53; Mismatches 105,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:AL132979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
96; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-370 < BLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: ATSP: F22013.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 96,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis C.Species: Arabidopsis thallana (mouse-ear cress)
C.Species: Arabidopsis thallana (mouse-ear cress)
C.Spate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C.Accession: T09911
R.Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Ma submitted to the Protein Sequence Database, June 1999
A.Reference number: 216896
A.Accession: T09911
                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                         195 PE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 VDDITEXCPREI-----ISLMKLCWEANPEARPTFPGIEEKFRPFYLSQLEESVEEDVK 302
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                                                                                                                                                                                                                                                                  303 SLKKEYSNENAVVKRMOSLOLDCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 ELHIKERVGAGSFGTVHRAEWHGSDVAVKILSIQ-DFHDDQFREFLREVCKQAVAIMKRV 726
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                                                                                                                                                                                                                                                                                                                                           143 LHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE-----GGTIIYMP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                Gaps
                                                                                                                     83
                                                                                                                                                     23 LDSGGFGKVSLCFH---RTQGLMIMKTVYKGPNCIEHNBALLEEAKMMNRLRHSRVVKLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLRE----AEILHKA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 LSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILHKARFSYIFPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 INE--ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLKK-----TKLQSV----SSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQ
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                                                          64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.310
A;Experimental source: cultivar Columbia; BAC clone T22A6
  Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                          Mismatches 146;
  ; DB 2;
3.3e-14;
  Score 369;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----POEENEPSLOSKLOD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 LHENSGSPETSRSLPAPQDNDFLSRKAQD 379
                                                          : 49
13.0%;
28.8%;
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                                                          Conservative
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A; Residues: 1-963 <BEV>
A; Cross-references: EMBI
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A;Map position: 4
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                                                       Matches 112;
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C;Accession: T52626
R;Jouannic, S.; Hamal; A.; Leprince, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.
Gene 229, 171-81, 1999
A;Title: Characterisation of novel plant genes encoding MEKK/STE11 and RAF-related pr
A;Reference number: 224447; MUID:99196996
A;Accession: T52626
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A;Note: F7H19.240
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A;Cross-references: EMBL:Y14199; NID:g2253009; PIDN:CAA74591.1; PID:g2253010
A;Experimental source: cultivar Columbia
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase homolog F7H19.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable mitogen-activated protein kinase MAP3K delta-1 [imported] - Arabido C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct_2000 #sequence_revision 24-Oct-2000 #text_change 08-Dec-2000
                                                 EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 -RFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 IMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674 VVGVVGFMDRRL-----DLPEGLNPRIASIIQDCWQTDPAKRPSFEELISQMMSLFR 725
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                                                                                 GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS-
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                                                                                                                                                                                                                                                                                        244 QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                              Length 736;
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A;Molecule type: mRNA
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Best Local Similarity 32.99
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A;Reference number: 216409
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Besidues: 1-370 <00E>
A;Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.10
A;Cross-references: cultivar Columbia; BAC clone F18B3
C;Genetics: A;Gene: ATSP:F18B3.10
A;Map position: 3
A;Introns: 54/2; 99/3; 164/1; 204/3; 257/3
A;Note: T3A5.110
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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A; Accession: T06576
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-982 < CHAC>
A; Residues: 1-982 < CHAC>
A; Residues: ERBL:AJ005077; NID:e1296722; PIDN:CAA06334.1; PID:e1296723
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable protein kinase TCTR2 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06576
R;Hackett, R.M.
submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 VAVKHLHIHT--PLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEF-HV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEP----GQKSRASIKHDIYSY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RMSSDSS-----IGTTL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       696 IPWEDLVIGERIGLGSYGEV---YHADWNGTEVAVK-----KFLDQDFSGAALAEFKRE 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 TLQRFWHSRPGPLDLKMSLSFAL--DISRAMEFVH--SNGIIHRDLNPRNLLVTGDLKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE-----RKDVLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Score 348.5; DB 2 29.2%; Pred. No. 2.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.0%; Score 340; DB 2; 30.8%; Pred. No. 2.5e-12; ive 56; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPDARPEFKEISVMLTNLLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P---VNHGPQEESCGSSQLHEN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 PDGEAYEGEMEESENSPLLOEH 334
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Best Local Similarity 29.2%
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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nes 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
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protein-tyrosine kinase (EC 2.7.1.112) 1 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Accession: T18276; A35670
B;Nuckolls, G.H.; Osherov, N.; Loomis, W.F.; Spudich, J.A.
B;Nuckolls, G.H.; Osherov, N.; Loomis, W.F.; Spudich, J.A.
A;Title: The Dictyostelium dual-specificity kinase splA is essential for spore differ A;Reference number: 218852; MUID:97053827
A;Reference number: 218852; MUID:97053827
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1584 <NUC>
A;Status: Drailinary; translated from GB/EMBL/DBJ
A;Residues: 1-1584 <NUC>
A;Cross-references: EMBL:U32174; NID:9974333; PID:9974334; PIDN:AAB41125.1
B;Tan, J.L.; Spudich, J.A.
Mol. Cell. Biol. 10, 3578-3583, 1990
A;Title: Developmentally regulated protein-tyrosine kinase genes in Dictyostelium dis A;Reference number: A35670; MUID:90287147
                                                                 hypothetical protein T16B24.18 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 17-Mar-2000
C; Accession: T02884
R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke submitted to the EMBL Data Library, August 1998
A; Reference number: Z14679
A; Reference number: Z14679
A; Reference number: Z14679
A; Ratus: translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Residues: 1-776 <ROUD
A; Residues: 1-776 <ROUD
A; Resperimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 2
A;Note: T16B24.18
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HN-MTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMP 194
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A;Residues: 'K',1249-1434,'L',1436-1584 <TAN>
A;Cross-references: GB:M33785; NID:g167775; PIDN:AAA33202.1; PID:g167776
A;Note: the authors translated the codon TAT for residue 271519 as Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HKLADLRYLSRGASGTVSSARHADWRYQVAVKHLHIHTPLLDSERKDVLREAEILHKARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.2%; Score 316.5; DB 2; Best Local Similarity 30.2%; Pred. No. 4.3e-11; Matches 87; Conservative 57; Mismatches 105;
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C;Keywords: ATP: phosphotransferase F:154-419/Domain: protein kinase homology <KIN>
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C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: S29851; S27760
R;Feng, X.H.; Zhao, Y.; Bottino, P.J.; Kung, S.
Biochlim. Blophys. Acts 1172, 200-204, 1993
A;Title: Cloning and characterization of a novel member of protein kinase family from shacesion: S29851; MUID:93176812
A;Accession: S29851
A;Molecule type: mRNA
A;Residues: 1-462 <FENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                            11;
                                                                                                                                                                                                                                                                                   RFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVN 133
                                                                                                                                                                                                                                                                                                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 VIHRDLKPENILIINEDNHLKIADFGI-----ACEEASCDLLADDPGTYRWMAPEMIK-- 331
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                                                                                                                                                                                                           DLQIGERIGIGSYGEVYRAEWNGTEVAVK-----KFLDQDFSGDALTQFKSEIEIMLRL 187
                                                                                                                                                                                                                                                                                                                                                                                                                         134 YLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVIN 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                               Gaps
                                                                                                                                         20 DLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE-RKDVL----REAEILHKA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKSRASIKHDIYSYAVITWEVLSRKOPFEDVTNPLQIMYS-VSQGHRPVINEESLPYDIP
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                                                                            33;
          Length 406;
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                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| || : : | : |: || || || : : |: |- : |: |- : |: |- : |: |- : |: |- : |: |- : |: |: |- : |: |: |- : |: |: |: |- : |: |: |- : |: |: |- : |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |: |: |- : |- : |: |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- : |- :
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11.6%; Score 327.5; DB.2; 32.1%; Pred. No. 4.5e-12; ive 50; Mismatches 107;
                                    Similarity 32.19
90; Conservative
                                                                        90;
   Query Match
Best Local S
Matches 90
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Best Local
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C;Genetics:
A;Map position: 4
A:Introns: 69/2; 107/3; 176/2; 194/3; 231/3; 289/2; 325/2; 350/1; 408/3; 440/3; 467/3
A;Note: F8020.290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dypothetical protein FBD20.290 - Arabidopsis thaliana CSPecies: Arabidopsis thaliana (mouse-ear cress) RSPECIES: TOTAL CACESSION: TOKE ROSE, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vossuphitted to the Protein Sequence Database, July 1998 ASPECIES: ASPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVEIPTDGTDEWEIDMKQLKIEKKVACGSYGELFRGTYCS--QEVAIK-----ILKPE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-----KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 PDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMM 173
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                                        ----GSAAWMAPEVFE---GSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMAAV
                                                                                                              SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTF----E
                                                                                                                                                      EI-------TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNH
                                                                                                                                                                                                                                                                                        297 PLOYPCOYSDEGOSNSATSTGSFMDIASTNTSNKSDTNMEQVPATNDTIKRLESKLLKNQ
                                                                                                                                                                                                                                                                                                                                                                                       |: || : || : || 357 AKQQSESGRLSLGASRGS--SVESLPPTSEGKRMSADMSEIE-ARIAATTGNGQPRRRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 WDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNP-LQIMYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 ACLNOSLD------ALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEF
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                                                                                                                                                                                                                                                                                                                                                  340 GPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 VAELDQDEKDQQNTSRLVQEHKKLLDENKSLSTYYQQCK 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 AKVIVQKLKD--NKQMGLQPYPEILVVSRSPSLNLLQNK
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Best Local S:
Matches 88;
                                                                                                              243
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      A Gene: splA
A:Introns: 47/3; 72/2
A:Introns: 47/3; 72/2
C:Superfamilty: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:1287-1566/Domain: protein kinase homology <</td>

        F;1295-1303/Region: protein kinase ATP-binding motif

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R. Sakurai, H.: Shigemori, N.; Hasegawa, K.; Sugita, T.
Blochem. Blophys. Res. Commun. 243, 545-549, 1998
A.Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind A. Reference number: UC5955; MUID:98153801
A. Accession: UC5955
A. Status: preliminary
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-579 cSAR>
A. Kesidues: 1-579 cSAR>
A. (Cross references: DDBJ:AB009356; NID:9224623; PIDN:BAA25025.1; PID:92924624
C.; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C. Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: i6-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KARFSYIFPILGICNE--PEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 LGVNYLHNMTPPLLHHDLKTQNILLDN------EFHVKIADFGLSKWRMMSLS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIMY-SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
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                                                                                                                                                                                                                                                      DB 2;
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| AJ278016 Homo sapiens mRNA for
| AF178953 Mus musculus receptor
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AF199466 Drosophila melanogast
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gb_in2:AF199466
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gb_in3:DDIDPYK1A
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                                                            Date: Jun 13,
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D49785 Rattus norvegicus mF
U32174 Dictyostelium discoi
ABO09356 Homo sapiens miNA
AJ005282 Homo sapiens mRNA
L13436 Homo sapiens guanyla
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Boldin, M. and Wallach, D.
MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL
SURVIVAL PATHWAYS
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Percent Identity: 100.000
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BOLDIN MARK (IL); WALLACH DAVID (IL)
Location/Qualifiers
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    8.3e-15
1.5e-14
7.3e-15
1.1e-14
1.3e-14
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A82777 GI:6732464
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. 452 c 449 g 539
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    413.37
408.85
414.29
411.34
409.77
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    313.50
313.50
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1210 TICAAGIGCCATICACCIAIGIGACAAGAAAAAAGGAAITAICICIGA 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 ISerSeralaileHisLeuCysAspLysLysLysMetGluLeuSerLeuA 334
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134 yrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGln 150
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                                                                                                                                                           660 ACCTGCACAATATGACTCCTCTTTACTTCATCATGACTTGAAGACTCAG
                                                                  AsnIleLeuLeuLespAsnGluPheHisValLysIlealaAspPheGlyLe
                                                                                                                                                                                                                                                                                                        710 AATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTTGGTTT
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                                                                                                                                                                                                               184 laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro
                                                                                                                                                                                                                                                810 CACCAGAAGGAGGACAATTATTATATGCCACCTGAAAACTATGAACCT
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1 (bases 1 to 1623)
MCCarthy,J.V., Ni,J. and Dixit,V.M.
RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase 98307936
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IPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRRAQDCYFWKLHHCPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RI 28-JUL-1998
2 (RIP2) mRNA, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="activtes NF-kappaB"
/function="induces cell death"
/note="RIP2; serine/threonine kinase homolog;
                                                                                                                                                    517
                                                                                                                                 484
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1610 ATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGA
                                                                                                                                                                                                          hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
                                                                                                                                                                                                                                                                                 PhealaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLe
                                                                                                                                                                                                                                                                                                      uGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnL
                                                                                                                                 pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
                                                         MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs
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LOCUS AF078530 1623 bp mRNA PR
DEFINITION Homo sapiens receptor interacting protein
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McCarthy, J. V., Ni, J. and Dixit, V.M.
Direct Submission
Direct (15-701-1998) Molecular On
Way, South San Francisco, CA 94080,
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1623
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/gene="RIP2"
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AF078530.1
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VERSION
KEYWORDS
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AUTHORS
TITLE
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euLeuGlnAsnLysSerMet 540

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301
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                                                                                                                                                                                                                                                                                                                                     Thome, M., Hofmann, K., Burns, K., Martinon, F., Bodmer, J.-L., Mattmann, C. and Tschopp, J. Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mattmann, C. and Tschopp, J.

Direct Submission
Submitted (12-MAY-1998) Institute of Biochemistry, University of '
Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066,
Switzerland
                                                                                                 AF064824 1902 bp mRNA PRI 07-JUL-1998
Homo sapiens CARD-containing ICE associated kinase mRNA, complete
                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1902)
Thome, M., Hofmann, K., Burns, K., Martinon, F., Bodmer, J.-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="CARD-containing ICE associated kinase"
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1545. :1811
/note="encodes CARD motif"
432 c 419 g 468 t 1
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2 (bases 1 to 1902)
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1601 TACTTCAAAATAAAAGCATG 1620
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AF064824.1 GI:3290171
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Ratio: 5.228
Percent Similarity: 100.000
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LOCUS AF064824
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267 rLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL 284
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                                                                                                                                              Pathlogy, Comprehensive Cancer & 1500 E. Medical Center Dr, Ann Arbor,
RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis J. Biol. Chem. 273 (20), 12296-12300 (1998)
                                                                                                                                                                                                                                                                                                              /gene="RICK"
225. 1847
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/note="CARD domain protein; phosphorylated protein"
                                                                                        Tobases 1 to 2501)
Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G. Direct Submission
Submitted (01-0CT-1997) Dept. Pathlogy, Comprehensive Cai Geriatrics Center, 4-131 CGGC 1500 E. Medical Center Dr. MI 48109, USA
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Gaps: 0
Percent Identity: 99.815
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1869
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1. .2501
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Ratio: 5.228
Percent Similarity: 100.000
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US-09-445-223-1 x AF027706
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete
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Inohara, N., del Peso, L., Koseki, T., Chen, S. and Nunez, G.
                                                                                                                                                                                                                                                                                                                              1143 ACTITICITGAAGCTGTTATTCAGCTAAAGAAAACAAAGTTACAGAGTGT 1192
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                                                    LeuHisGluasnSerGlySerProGluThrSerArgSerLeuProAlaPr 367
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LOCUS AF027706
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AF027706.1
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                                   yrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGln 150
                                                                                                                                                                                          AsnileLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLe 167
                                                                                                                                                                                                            724
aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT 134
                                                                          101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro
                                                                                                                                                                                                                                                                              CACCAGAAGGAGGACAATTATCTATATGCCACCTGAAAACTATGAACCT
                                                                                                                                                                                                                                                                                                          GlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaVa
                                                                                                                                                                                                                                                                                                                      217 lilethtTrpGluValLeuSerArgLysGlnProPheGluAspValThrA
                                                                                                                                                                                                                                                                                                                                                            TATCACATGGGAAGTGTTATCCAGAAAACAGCCTTTTGAAGATGTCACCA
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Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 116550)
Ozersky,P., Holmes,A. and Broy,M.
The sequence of Homo saplens BAC clone CTA-437L15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
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Park Avenue, St. Louis, Missouri 63108,
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complete sequence.
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allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
                                                     ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly
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AC004003
AC004003.1 GI:2772557
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Submitted (15-JAN-1998) Do
University, 4444 Forest Pa
3 (bases 1 to 116650)
Waterston,R.
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University, 4444 Forest
4 (bases 1 to 116650)
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Waterston, R.
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LOCUS AC004003 116650 bp
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Direct Submission
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21552. .21601,22478. .22639,29890. .29975,33855. .33944,
36395. .36488,39123. .39284,39881. .40218)
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone CTA-437L15 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from VECTOR: pBeloBAC11
                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is CTA-237G1. The actual start of this clone is at base position 1 of CTA-437L15; actual end is at 116650 of CTA-437L15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmmc.org) at the Virginia Mason Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted:
                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone contains STS HS275YF1 (NID:g1051703).
Location/Qualifiers
1. .116650
                                                                                                                                  Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                                               Center project name: H_RG437L15
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gene="WUGSC:H_RG437L15.1"
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150. 530
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                                                          ---- Genome Center
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845. .4563
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/rpt_family="MaLR"
3188. .3348
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110. pri
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KIADFCLSKURMASLSQSRSSKSAPEGGTIIYMPPENYEPGGKSRASIKHDIYSYAVI
TWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQN
DDRPSFEKKCLIELEPVLRTREEIFFRANTOLKKTKLQSVSSAIHLCDKKKRELSLN
IPVHHGPOEESCGSQLHENGSPFFISSLPAPQDNDFSRKAQOYFWKLHHCPGNH
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MTEACLNQSLDALLSRDLJMKEDYELVSTKPTRTSKVRQLLDTTDIGGEEFAKVIVQK
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/note="serine/threonine kinase RICK; match to protein AP027706 (PID: 93123887) and mRNA AF027706 (NID: 93123886); H_RC437L15.1"
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                                                                                     /evidence=not_experimental
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26151. .26280
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26611. .27000
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A 39574	. 428	A 39624	. 428	T 39674	. 428	C 39724	. 428	Т 39774	. 428	т 39824	. 428	т 39874	s 443 39924	ie 460 - :r 39974	tv 477 	nr 493 17 40074	.y 510 40124	.s 527 			13-JAN-1999 snce.	orata; Euteleostomi; Inidae; Homo.	itute of Molecular 15, Germany 11g. The start of this
5 AAGTTATTTTTGTTTAATTTAACAAATTTGCAGGTATCTTTTATATTTGAA		5 ATAAAATGGACATCAAACAAAACTGAACAAATCCCAGAAGATGGGAATGA		5 TGACATAAAGTGGTTTTTGCCCCGTGATTTATACCATAGGAAAAGGCAGT		5 GCCTTTTCT		5 TGAAAATG		5 CATAGGAAAATTATGTTTTATGCTTTATTTTTTTTTTGATGGAATTTTACT		5 TATTGCTATGTATCTGTCCTCACCTTTTAAATTATTCATTC	9GluargLeuGlnProGly1lealaGlnGlnTrp1leGlnSerLys :::	4 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLe	0 uaspalaLeuLeuSerArgaspLeuIleMetLysGluaspTyrGluLeuV	. ~ 10	-1 10		7 erargSerProSerLeuasnLeuLeuGlnasnLysSerMet 540 	le: gb_pr4:AF117829	seq_documentation_block: LOCUS AF117829 320250 bp DNA PRI 13-JAN-1999 DEFINITION Homo sapiens 8q21.3: RICK gene, complete sequence. ACCESSION AF117829 VERSION AF117829.1 GI:4151947 KEYWORDS HTG. SOURCE human.	IISM Homo sapiens Eukaryota; Metazoa; Chordata; Cranlata; Verte Eukaryota; Metazoa; Chordata; Catarrhini; Hom Mammalia; Eutheria; Primates; Catarrhini; Hom (CE 1 (bases 1 to 320250) RRS Platzer, M. and Varon, R.	Unrect Submission (A) Submitted (30-DEC-1998) Genome Analysis, Inst Biotechnology, Beutenbergstrasse 11, Jena 077 This sequence is part of a larger genomic con commonce is directed towards the centromere.
39525	428	39575	428	39625	428	39675	428	39725	428	39775	428	39825	429 39875	444 39925	3997	47	494	510	527	sed_name	seq_docus LOCUS DEFINITI ACCESSIG VERSION KEYWORDS	ORGANT REFERENC AUTHOI	TITLE JOURNI COMMENT

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44	ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLe 4	09
Φ		79543
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SOURCE	house mouse.	

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GCCCGAGTCCTCACGCCTCAAGCGCGCGCTCTGCTTCGCTTCGATAACG 1040
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                                                                                                                                                                                                                                                                                                                                                                                                      erArgLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyr 240
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  288 ACATICTACCIGIGIACCGCATAIGCCAGGAACCI.....GICGGCIIG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 InSerArgSerSerLysSerAlaProGluGly.....GlyThrileIle 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rIleLysHisAspIleTyrSerTyrAlaValIleThrTrpGluValLeuS 224
                                                                                                                                 G......CCATTGCCTTGGGACCTGCGCTTTCGCATCGTGCACG
                                                                                                                                                                                                                                                570 AGGACCTCAGCATG......GATGGCCTGTTTGGTACAATCGCT
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LQGKDAWLPLHYAAWQGHLPIVKLLAKQPGVSVNAQTLDGRTPLHLAAQRGHYRVARI
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901 c 1000 g 83.2 t
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FEREASTGDLGPTDIQKKKLVDAIISGDTSRLMKILQPQDVDLVLDSSASLLHLAVEA
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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A., Rowitch, D. and Pillai, S. PRK, a novel ankyrin repeat-containing protein kinase regulated by protein kinase C-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKKPFADEKNILHIMMKVVKGHRPELPPICRPRPRACASLIGLMQRCWHADPQVRPTF
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                                                                                                                                          Unpublished
Unpublished
(bases 1 to 3559)
Chen,L., Haider,K., Cariappa,A. and Pillai,S.
Direct Submission
Submitted (01-SEP-2000) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
Location/Qualifiers
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AUTHORS
TITLE
                                                                                                                                               JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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257

871

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ babr, C.; Rohwer, A., Stempka, L., Rincke, G., Marks, F. and Gschwendt, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIK, a Novel Protein Kinase That Interacts with Protein Kinase Cdelta. CLONING, CHARACTERIZATION, AND GENE ANALYSIS J. Blol. Chem. 275 (46), 36350-36357 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1125 CCTCTG.....AATGCAAGCTCCCATCGTCCAGCAGTGGCAAG 1162
                                                                                                                                                                                                                                                                                                                                                                                             1323 TGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTCTAGACAGCAGTGCC 1372
                                       1062 .rgr......cacagrrgg......acrcrgggarcrcccagac 1092
                                                                                                                             .........AAGGCCCCGAAGAGCTCAGCCGAAGTT... 1124
                                                                                                                                                                                                                                                                                                          1163 AGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTTTCCTCCAGAG.... 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 lnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerPro 530
                                                                                                                                                                                                                                                                  437 n.....GlnTrpIleGlnSerLysArgGluAspIleV 448
                                                                                                                                                                                                                                                                                                                                                      448 alAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeu 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 oThrArgThrSerLysValArgGlnLeu..LeuAspThrThrAspIleGl 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 nGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                          465 SerArgAspLeulleMetLysGluAspTyrGluLeuValSerThrLysPr 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSA278016 3879 bp mRNA PRI
Homo sapiens mRNA for protein kinase (dik gene).
AJ278016
387 sCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgA
                                                                                                                                                                            421 ProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGl
                                                                                          404 laalaPheCysAspHisLysThrThrProCysSerSerAlaIleIleAsn
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dlk gene; protein kinase.
human.
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Gschwendt, M.
                                                                                                                                                                                                                                                                                                                                                                                                .....GATCGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_pr8:HSA278016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1373 AGCCTG 1378
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                                                                                                                                    1093 TCTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1230 AGC
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 IleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrPr 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 ATCATCCACGAGAGGGGGGGGGGGATGAACTTCCTGCACTGCATGGCCCC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 oProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 luPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMet 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 TGGCTTCGGAG......CCATTGCCATGGGATCTCCGGTTCCGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 ACTACCACGTCAAGATTTTGTGATTTTGGTCTGGCCAAGTGCAACGGGCTG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 eLeuGly11eValThrGluTyrMetProAsnGlySerLeuAsnGluLeuL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 euHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 GCTGGCCATCAAGTGCTCGCCCAGCCTGCACGTCGAC......G 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 spSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 ArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluPh 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 GlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG1 43
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Gaps: 25
Percent Identity: 32.762
                                                                           /evidence-experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ģ
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1.913
54.667
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Ratio:
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CDS
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188 596	205	220	237	254	266 825	283	300	316	328 935	345 985	361 1009	378 1043	394	411	425	442	458	1173
4 SerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyGl	nTyrG : : CATCAC	5 rgalaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTrp :::	1 GluvalLeuSerargLysGlnProPheGluAspValThrAsnProLeuGl 	7 nIleMetTyrSerValSerGlnGlyHiSArgProValIleAsnGluGluS:	4 erLeuproTyrAspileProHisArgalaArgMetile :: 6 AGCTGCCCCCGTGTGCAGAGCCGGCGGCGCGCGCGCCTGAGTA	7 SerLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPh	3 eLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluI ::: 1ACCTTCCAAGAAA	heLeuGluAlaValIleGlnLeuLysLys [;]		SMETGLULEUSETLEUASNILEPTOVALASNHISGLyPTOGLNGLUS	5 er.CysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSe 	AlaProGlnAspAsnAspPheLeuSerArgLy ::: CGACCTTCGATAACGACTAC	HisHisC	:lySerGlnArgAlaAlaPhe ::: \GGCTGTCGAGGGCC	snProLeuSer :: srccaacreca	<pre>5 aGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnS</pre>	41	3
17	18	20	22	23	25	26	28	30.	31	32	34 98	36 101	37	39	41	42 114	44	117

439 SE 11 1174 TC	Settlementsphaletteusestatgaspheulitemettyseluasphyris. 4/5 ::: ::: ::: ::: ::: ::: :::
475 uL 1224 G.	uLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuA 492
492 sp 1250 GT	spthrThraspileGlnGlyGluGluPhealaLysValIleValGlnLys 508
509 Le 1300 GA	LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuVa 525 :::::
525 lv :: 1350 AC	IValSerArgSerProSerLeu532:::::::: ACTGGACAGCGGCCAGCCTG1371
sed_name: g	eq_name: gb_rol:AF178953
seq_documen LOCUS DEFINITION	sed_documentation_block: LOCUS AF178953 1833 bp mRNA ROD 19-OCT-1999 DEFINITION Mus musculus receptor interacting protein 3 (Rip3) mRNA, complete
ACCESSION VERSION	cds. AF178953 AF178953.1 GI:6063100
SOURCE ORGANISM	house mouse. Mus musculus
H CNG GG GG	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1, Asaca 1 to 1833.
AUTHORS	Pazdernik, N.J., Doner, D.B., Goebl, M.G. and Harrington, M.A. Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting or a Debth Domain but Induces Apoptosis and Activates NF-kapaB
JOURNAL	Mol. Cell. Biol. 19 (1999) In press
AUTHORS	Pazdernik, N.J., Donner, D.B., Goebl, M.G. and Harrington, M.A. Direct submission
JOURNAL	Submitted (19-AUG-1999) Walther Oncology Center, Indiana University School of Medicine, 1044 West Walnut Street, Indianapolis, IN 46002. ISA
FEATURES	,
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	u
DASE COUNT ORIGIN	400 a 497 C 477 g 593 C

alignment_scores:

279 295 1011 307 1061 323 11111 323 11111 327 11211 357 1298 403 1298 403 1298 403 1298 403 1298 403 1298 403 1298 403 1298 408 408 406 406 406 406 406 406 406 406 406 406	04-FEB-1998
62 9AlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspG 30 GGAAAAACTGAAGAGACTTAATTCATTGCTGGGGTTCCCGGAAA 79 luArgProSerPheLeuLySCySLeuIleGluLeuGluProValLeuArg 180 ACAGGCATCCTCCAGGACTGC 181	1499 T 1499 seq_name: gb_pat2:168122 seq_documentation_block: Locus Locus DEFINITION Sequence 14 from patent US 5674734.

us-09-445-223-1.p2n.rge

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168122.1 GI:2830244 168122.1 GI:2830244 1 Unknown. ISM Unknown. Unclassified. Unclassified. Unclassified. I (bases 1 to 2268) SE Leder.P., Seed.B., Stanger,B.Z., Lee,T. and Kim,E. Cell death protein AL Patent: US 5574734-A 14 07-OCT-1997; Location/Qualifiers 1. 2268 Arganism="unknown" Arganism="unknown" Arganism="unknown" Arganism="unknown"	alignment_scores: Quality: 397.00	seg 1/1 to: 168122 from: 1 to: 2268	LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr 40 ::: ::: ::: ::: CTAGACAGCGGAGGCTTCGGGAAGGTGTCCTTGTGTTACCACAGAAGCCA 167	<pre>pargValGlnValAlaValLySHisLeuHisIleHisThrProLeuLeuA 57 ::: </pre>	spSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLys 72 	3 AlaargPheSerTyrIlePheProIleLeuGlyIleCysasnGluProGl 89	<pre>uPheLeuGlylleValThrGluTyrMetProAsnGlySerLeuAsnGluL 10 ::::: </pre>	<pre>6 euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 12 :: </pre>	ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh	<pre>rProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspA 1 ::::: .:: .:: </pre>	snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 177 ::::: ::	Metser. TGGAGCA	6GluGlyGlyThrIleIleTyrMetProProGlu. 19 :::	7
VECESSION VERYWORDS SOURCE ORGANISM ORGANISM TITLE JOURNAL FEATURES SOURCE SOURCE BASE COUNT	alignment Percent alignment	Align s	24	40	57 209	73	99	106 359	123	139	156 494	173	186 594	197

644	ACCTGAATGACATCAATGCAAAGCCCACGGAGAAGTCG 6	681
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316	rValSerSerAlaIleHisLeuCys	324
325	Den[welwewott] nfonCorlonaenI obroVe) henU(ef) v	• <
ı L	ATTCAGAACAACCTGGATCGCTGCACAGTTCCCAGGGGCTCCAGATGGGT	r
341	ProGlnGluGluSerCysGlySerSerGlnLeuHisGl	353 1154
353	uAsnSerGlySerProGluThr	360
1155	GAATGATCGCAGTGTGCAGGCTAAGCTGCAAGAGGAAGCCAGCTATCATG	1204
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371 1255	AspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuH1sH1 ::: :: :: :: GAGGCTTACAACAGAGGAGGAGGAAGGAAACGAAGGGTCTCTCA	387 1298
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406	PheCysAspHisLysThrThrProCysSerSerAlalleIleAsn	420
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421	ProLeuSerThrAlaGlyAsnSerGluArgLeuG 4	432
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432	lnProGly1leAlaGlnGlnTrpIleGlnSerLys	443
1490	CGCCAAATCTAAGCCAAATGTATAGTACTTATAAAACTCCAGTGCCAGAG	1539

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LWAFFARKEPPENVICTEGPVICIIKSGNRPNVEBILEYCPREIISLMERCWQAIPEDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mQPDMSLDNIKMASSDLLEKTDLDSGGFGKVSLCYHRSHGFVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanger, B.2., Leder, P., Lee, T.H., Kim, E. and Seed, B. RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (CD95) in yeast and causes cell death Containing and causes cell death (CP) 513-523 (1995)
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2268)
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Locus MMU25995 2268 bp mRNA ROD 24-MAY-1995
DEFINITION MAS musculus cell death protein (RIP) mRNA, complete cds.
ACCESSION U25995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell death'
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1740 CACCACTAGTCTGATCTGATCTGAACCTGG 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1790 GAAGGCAGTGGAAAACTGTGCCCGCAAGCTGGGCTTCACTGAGTCTCAG 1839
                                                                                                                                                                                                                                                                                            1640 TIGGAAACCACAATTATATGGATGTTGGACTGAATTCACAACCACCAAAC 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                      507
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02115, USA
                                                                                                                                  1590 AGCAGATGACCTCATAAAATATACTATATTCAATAGTTCTGGTATTCAGA
                                      1540 ACCAACATACCGGGAAGCACACCCACCATGCCATACTTCTCTGGGCCAGT
                                                                                                                                                                             452 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLe
                                                                                                                                                                                                                                                                      468 ulleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrS
                                                                                                                                                                                                                                                                                                                                                               485 erLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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/clone="III2"
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                                                                                         444 .ArgGluAspIleVal.AsnGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 nLysLeuLysAspAsnLysGlnMet
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52. .2022
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Fas; TNF receptor.
house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_rol:MMU25995
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95277838
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KEYWORDS
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443
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FSGPVADDLIKYTIENSSGIQIGNINYMDVGLNSQPPNNTCKEESTERHQAIFDNTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594 CACCACTAAGAAGAAGAAGGTGGTACCCTTTACTACATGGCACCCGAAC 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 GAACTATICGCIGGIGAIGGAGIACAIGGAGAAGGGCAACCIGAIGCACG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 TGGATTTGTCATCCTGAAAAA.....GTATACACAGGGCCCAACC 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AGGATAATCGTGGAGGCCATAGAAGGCATGTGCTACTTACATGAC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 609
Gaps: 25
Percent Identity: 25.452
                                                                                                                                                                                                                                                                                       /gene="RIP"
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490 c 577 g 482 t
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                                                                                                                                                                              /gene="RIP"
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51.232
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US-09-445-223-1 x MMU25995
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208	225	242	256 825	273 857	290	305 954	316	324 1054	340	353 1154	360 1204	370 1254	387 1298	389 1348	405	420	432 1489
97	209 LysHisAspIleTyrSerTyrAlaValIleThrTrpGluValLeuSerAr :::: ::::::::: G82GACGTGTACAGCTTTGGCATTGGCCAATATTTGCAAA	225 gLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerV 	242 alSerGlnGlyHisArgProValIleAsnGluGluSerLeuPro :::::::: :::	257 TyrAspileProHisArgAlaArgMetileSerLeuileGluSerGlyTr 	palaginasnproaspgluargproserPheLeuLysCysLeuilegluL 	290 euGluproValleuargThrpheGluGlulleThrPheLeuGluAla :::::	306 ValileGlnLeuLysLysThrLysLeuGlnSe	316 rValSerSerAlalleHisLeuCys	325AspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGly ::::::: 1055 ATTCAGAACAACCTGGATCGCTGCACAGTTCCCAGGGGCTCCAGATGGGT	341 ProglnGluGarCysGlySerSerGlnLeuHisGl	3 uasnSerGlySerProGluThr	361SerārgSerLeuProalaProGlnāspāsn 205 CTTTGGAATATTTGCAGAGAACAGACAAAACGGCGGCGAGCAGATAT	371 AspPheLeuSerargLysalaglnaspCysTyrPheMetLysLeuHisHi ::: :: ::::	387 scyspro	390GlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAla :::		ProLeuSerThralaglyAsnSerGluArgLeuG
19	6 17	2	7	C1 00	27.	0 O	m oi	3	32	34.	35.	3	3	3	13	13	421

	432 InProGlyIleAlaGInGInTrpIleGInSerLys	1540 ACCAACATACCGGGAAGCACACCCATGCCATACTTCTCTGGGCCAGT 1589 444 .ArgGluAspIleVal.AsnGlnMet	ulleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrS 485 :::	507 nLysLeuLysAspAsnLysGlnMet 515 :::::: :::::	seq_documentation_block: DNA PAT 14-FEB-2001 LOCUS AR105328 1557 bp DNA PAT 14-FEB-2001 DEFINITION Sequence 2 from patent US 6096539. AR105328 VERSION AR105328 AR105328. CENTROLING AR105328. CENTROLING AR105328. CENTROLING CENTR	Unclassif Unclassif 1 (bases Gomes, B.C Protein a Patent: U	BASE COUNT 395 a 422 c 448 g 291 t 1 others ORIGIN Alignment_scores:	alignment_block: US-09-445-223-1 x AR105328 Align seg 1/1 to: AR105328 from: 1 to: 1557	rileProTyrHisLysLeualaaspLe	27 yalaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnV 44 :::	44 alAlaValLySHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60
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	DOTTCG	162	
61 LysAspValLeuArgGlu ::: 63 AAGGCGATATCCAGGGA	LysaspValțeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy ; ::: :::: AAGCGATATCCAGGGAGGTCAAGGCCATGGCAAGTCTGGATAACGAATT ;	77 212	
77 rilePheProileLeuG] 	rIlePheProlleLeuGly11eCysAsnGluProGluPhe	90	
91LeuGlyIleVal: ::::: 63 CCAAGCCGGCTCTGGTG	LeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGlu : .:::: ::::: CCAAGCCGGCTCTGGTGACTAATTCATGGAGAACGCTCCTTGTCGGGG	105 312	
06 LeuLeuHisArgLysThrGluTyrPro :: :: 13 CTGCTGCAGTGCCGTYGGCCCT	AspValAlaTrpProLeuArgPh TGGCCGCTTTG	122 353	
22 eArgileLeuHisGlui ::: : 54 CCGCCTGCTGAAAGAAG	eArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetT	139	
39 hrProProLeuLeuHis ::[hrproproleuLeuHisHisAspLeuLysThrGlnAsnileLeuLeuAsp:::	155 453	
56 AsnGluPheHisValLy :::	AsnGluPheHisValLysIlealaAspPheGlyLeuSerLysTrpArgMe ::: :::	172 501	
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122 lLeuSerArgLysGlnP :: 	LeuSerArgLysGlnProPheGluAspValThrAsnProLeuGlnIleM ::: ::::: CTTGCTGGAAGAGAAGTTGAGTTGCCAACCGAACCATCACTGGTGT	239	
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268 ulleGluSerGlyTrpA ::::: 783 AATGCAGCTCTGCTGGA	ullegluserglyfrpalaglnasnbroaspgluargproserpheLeuL :::::: ::::::: :::	285 832 ·	
285 ysCysLeulleGluLeu ::1 333 AATGCCTACCAAAACT	yscysLeulleGluLeuGluProValLeuArgThrPheGluGluIleThr :: :: :: :::	301 876	
302 PheLeuGluAlavalll ::::: ::::: 377 AATATGAATGCTGCTGT	PheLeuGlualaValIleGlnLeuLysLysThrLysLeuGlnSerVälse :::::: :::::::	318 926	
318 rSer.alaIle 927 GAGCAGCAATAGGAGAI	rSer.AlaileHisLeuCysAspLysLysMetGlu	330 976	
331LeuSerLeuAs	LeuSerLeuAsnIleProvalAs	338	

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Homo.

Eukaryota; Ho
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                                                                     1253 Greergeaccecgaggaareaggggergagag......1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1329 AGTAACAGGGCGACCGCTCGTTAACATATACAACTGCTCTGGGGTGCAAG 1378
                                                                                                                                                                                                                                                                   1153 GCAGGCACATCTTCAGATTCGATGGCCCAACCTCCCCAGACTCCAGAGAC 1202
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977 AAATGGATGGCTTTAGGAGAACCATAGAAAACCAGCACTCTCGTAATGAT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 .....GlnAsp 379
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                                                                                                                                                                                                                            351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 367
                                                                                                                                                                                                                                                                                                                                                                               367 oGlnAspAsnAspPheLeuSerArgLysAla......
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Gaps: 21
Percent Identity: 28.056
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LOCUS AX067677 1557 bp DNA
DEFINITION Sequence 2 from Patent WO0077200.
ACCESSION AX067677
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US-09-445-223-1 x AX067677
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Ratio:
Percent Similarity:
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us-09-445-223-1.p2n.rge

11 ProthrileProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGl 2	27 89 44
CGGGTTCGGCACAGTGTTCCGGGCGCAACATAGGAAGTGGGGCTACGATG alalavalLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg. IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	139 60 162
	77 212
77 rIlePheProlleLeuGlyIleCysAsnGluProGluPhe	90
91LeuGlylleValThrGluTyrMetProAsnGlySerLeuAsnGlu 1 ::::: ::: 263 CCAGCGGCTCTGGTGACTAAATTCATGGAGAACGGCTCCTTGTGGGG 3	105
106 LeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPh 1	122 353
122 eArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetT	139
139 hrProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAsp 1 ::	න ප න ද
156 AsnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMe 1 :::	172
172 tMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyGlyT 1 :::	189 544
189 hrIleIleTyrMetProProGludsnTyrGluProGlyGlnLysSerArg 2	205 591
206 AlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTrpGluVa 2	222 641
222 lLeuSerargLysGlnProPheGluAspValThrAsnProLeuGlnIleM 2	239
239 etTyrSerValSerGlnGlyHisArgProVallleAsnGluGluSer 2 ::: :::: :::	254 732
255 LeuproTyrAsplieProHisArgAlaArgMetlleSerLe 2 	268 782
268 ullecluserGlyTrpAlaGlnAsnProAspGluArgProSerPheLeuL 2 	285 832
285 ysCysLeulleGluLeuGluProValLeuArgThrPheGluGlulleThr 3 :: :: ::: :::	301 876
	318

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14-FEB-2001
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Worknown.

JE 1 (bases 1 to 1873)

S Gomes, B. Charles, Kasof, G.M. and Prosser, J. Caroline.

Protein activator of apoptosis

Notein activator of apoptosis

Location/Qualifiers

Justin 1.873

Justin 1.873

Jorganism="unknown".

531 c 518 g 353 t
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1329 AGTAACAGGGGGACCGCTCGTTAACATATACAACTGCTCGGGGTGCAAG 1378
                                                                                                                                                  1153 GCAGGCACATCTTCAGATTCGATGGCCCAACCTCCCCAGACTCCAGAGAC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1027 GTCATGGTTTCTGAGTGGCTAAACACAGATCTAGAGGGGGGCCTCCCAG 1076
                                                                                                                                                                                                                                                                                                                                                                          1203 CTCAACTTTCAGAAACCAGATGCCCAGCCCTACCTCAACTGGAACACCAA 1252
                                                                                                                                                                                                                                                                                                                                                                                                                      378 .....GlnAsp 379
                                                                          331 .....LeuSerLeuAsnIlePro.....valAs 338
                                                                                                                                                                                                   338 n.HisGly.....ProGlnGluGluSerCysGlySerSerGln 350
                                                                                                                                                                                                                                                                       351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 367
                                                                                                                                                                                                                                                                                                                                               367 oGlnAspAsnAspPheLeuSerArgLysAla......377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 CysTyrPheMetLysLeuHisHisCysPro......GlyAsnHi 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 sSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 isLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAla 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 GlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSe 442
318 rSer.AlaIle.....HisLeuCysAspLysLysLysMetGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 rLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
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Gaps: 22
Percent Identity: 28.144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR105327 1873 bp DNA
Sequence 1 from patent US 6096539.
AR105327
AR105327.1 GI:12818924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392.50
1.443
54.291
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TITLE
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		283 het.e.
alignment_block US-09-445-223-	L_DIOCK: 45-223-1 x AR105327	
Align s	seg 1/1 to: AR105327 from: 1 to: 1873	
11	ProthrileProtyrHisLysLeualaaspLeuargTyrLeuSerArgG1 27	
27	valaserglvThrValserSerAlaArgHisAlaAspTrpArgValClnV	
254		1088 GCTC
44	alalavalLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60	1138 GGAC
304	TGGCGGTCAAGATCGTAAAC	337 .Val.
327		
77 377	rllePheProileLeuGlyile	
87	IUProGluPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeu 103 	
104		
120		
137		390 yAsn :::: 1414 CACC
154	 LeuAspasnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTr 170 	1454
170	<pre>pargMetMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluG 187 :::: </pre>	
187	1yGlyThrIleIleTyrMetProProGluasnTyrGluProGlyGlnLys 203 ::: :: ::: ::: :::	1540 TGCP
204	 SerArgalaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTr 220 :: 	seq_name. yb_
220		ACCESSION P VERSION P KEYWORDS
237	7 InIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGlu 252 ::: ::: ::::: :: ::: 0 TCGTGTACGAAGCAGCAACAGGCAGAACCGGCCTTCATTGGCTGAG 899	ORGANISM
253	3 GluserLeuProTyrAspIleProHisArgAlaArgMet11 266	AUTHORS TITLE JOURNAL
26	266 eSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerP 283 ::: :::::: 944 ggagntaAnggaggaggaggaggagggagggagggagggagggagg	FEATURES SOURCE

6 6 6 6 6 7	336 1187 348 1237 365 1263 377 1313	390 1413 407 1453 1489 440 1539 156	19-JAN-2001 ta; Euteleostomi; idae; Homo.
a . 0 et a — 13	GGACAGAAATGGATGGTTTAGGAGAACAGAAAAACAGAATTCGT	LLYSLeutlishisCysPro	itation_block: Ax067676 Ax067676 Ax067676 I873 bp DNA PAT 19 Sequence 1 from Patent WO0077200. Ax067676 Ax067676 Ax067676.1 GI:12329570 human. Homo sapiens Edwarycta; Metazoa; Chordata; Craniata; Vertebrata; Edwarycta; Metazoa; Chordata; Catarrhini; Hominidae; Comesynca; Eutheria; Primates; Catarrhini; Hominidae; Comesynca; Lot 1873 Receptor interacting protein rip3 Patent: WO 0077200-A 1 21-DEC-2000; AstraZeneca AB (SE) AstraZeneca AB (SE) 1. 1873 Acrganism="Homo sapiens"
	331	378 GlnAspCysT 1364 AGAGACCTC? 390 YASHISSEI 1114 CACCAAGTC 407 YSASPHISL, 1454 1490 AAATCCAGTY 440 eGInSerLys	ame: gb ocument ITION SION ON ON ON EE E E ANISM HORS HORS HORS HORS RNAL RRES
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87 luProGluPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeu 103 104 AsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLe 120 170 pargMetMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluG 187 187 lyGlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLys 203 SerArgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTr 220 pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG 237 237 InIleMetTyrSerVal...SerGlnGlyHisArgProValIleAsnGlu 252 ::: ::: ::: ::: |||| 11 ProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGl 27 27 yAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnV 44 61 LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 77 44 alAlaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60CysAsnG 87 Length: 501 Gaps: 22 Percent Identity: 28.144 353 to: 1873 /db_xref="taxon:9606" 1 531 c 518 g from: 1 77 rilePheProileLeuGlyile..... 392.50 1.443 54.291 Align seg 1/1 to: AX067676 alignment_block: US-09-445-223-1 x AX067676 471 a Quality:
Ratio:
Percent Similarity: alignment_scores: BASE COUNT ORIGIN 427 907 204 220 803

456 1588	0 eGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu	154(
1539	::::::	1490
440		424
1489		1454
423	ysAspHisLysThrThrProCysS	407
1453		141
407) yAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheC	390
1413	::	136
390		378
1363	TGGACAGCACATCTTCAGATTCGATGGCCC	1314
377		377
1313		1264
377	AsnAspPheLe	36
7		(7)
365		346
346	valash: hisselyriosine usercysely ser ::: 11111 ::: 111111	118
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336	1LeuSerLeuAsnIlePro	33.
1137	::::	1088
330	rV.	316
1087		104
316	11	300
1040	1 ::: ::: 4 TCCAGGAATGCCTACCAAAAACTGATGATGATGTTCCAGATGGTGGAG	766
299		283
993		94
283		. 266
943	::: ::	900
266	GluSer	253
899	0 TCGTGTACGAAGCAGTGTGCAACAGGCAGAACCGGCCTTCATTGGCTGAG	82(

9e-18 9e-18 3e-18

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can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B1 protein; intracellular mediator; modulator; inflammation; cell deatn; cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
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       468.19
464.87
464.87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes the isolation of a novel human B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
       312.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 649 A; 452 C; 449 G; 539 T; 9 other;
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Gaps: 0
Percent Identity: 100.000
   /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:T85095 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT:X56279 + /cgnl_8/gcgdata/geneseqn/NA2000.DAT:X35105 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT:X99696 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:X9324 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:010324 +
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97IL-0121011.
97IL-0121199.
                                                                                                                                                                                                                                                                                                                               X02558 standard; cDNA; 2098
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Ratio: 5.239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B1 cDNA
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-Q-Cgnl_1/USPTO_spool/US09445223/runat_13062001_092033_29676/app_query.fasta_1.604
-Q-Cgnl_1/USPTO_spool/US09445223/runat_13062001_092033_29676/app_query.fasta_1.604
-DEABLY-d.000 -QRAPET-6.000 -LOOPCL-0.000 -LOOPEXT-0.000
-QAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.500
-GAPOP-4.500 -GGAPEXT-0.000 -XGAPOP-10.000 -XGAPEXT-0.500
-GAPOP-6.000 -GAPEXT-7.000 -START-1 -MATRIX-bloomColored
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_AMAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
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OM of: US-09-445-223-1 to: N_Geneseg_0401:*
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length: 291890651
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Query: US-09-445-223-1
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phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder; ss.
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                                     1510 ANTANTAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTG
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                                                                          oGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetL
                                                                                    ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly
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84 leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human phosphorylation effectors useful for the diagnosis, treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46138-246168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                              Baughn MR;
H, Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and prevention of proliferative, immune and neuronal disorders
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                                                                                                                                                                                                                                                                                                                          Lal P, Tang YT, Corley NC, Guegler KJ, Bandman O, Au-Young J, Gorgone GA, Yue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 other;
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                                                                                                                             98US-0152814.
98US-0173482.
98US-0106889.
                                                                                                                                                                                      98US-0109093.
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                                                                        99WO-US17132
                                                                                                             98US-0123494
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Patterson C, Bandman O, A
Reddy R, Lu DAM, Shih LL;
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Percent Similarity: 100.000
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WO200006728-A2
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19-NOV-1998
                                    10-FEB-2000
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1203 ACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAG 1252
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453 TITGCAAIGAGCCTGAAITTITGGGAAIAGTIACTGAAIACAIGCCAAAI
                                                                    aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT
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Quality: 2823.00
Ratio: 5.228
Percent Similarity: 100.000
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US-09-445-223-1 x C77779
              Rosen CA, Ruben SM;
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dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopolatic cell disorder; attoimmune disorder; altoimmune disorder; altoimmune disorder; haematopolatic cell disorder; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer associated gene; cancer antigen; detection; cancer;
                                                              1653 CCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAA 1702
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                                                                                                                                                                                                     434 lyileAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGln 450
                                                                                                                                                                                                                                                                     MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs 467
                                                                                                                                                                                                                                                                                                                                         pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT 484
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                                                                                                                                                                                                                                                                                                                                                                                                          484 hrSerLygValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uGlnProTyrProGlu1leLeuValValSerArgSerProSerLeuAsnL
384 ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly
                                                                                                                                    417 allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated gene sequence SEQ ID NO:173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C77779 standard; cDNA; 2709 BP
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451 1553 467

C77779;

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C77607 to C78448 encode the human cancer associated proteins given in and calls the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antidiasthmatic; antidiabetic; antidiasthmatic; antidiabetic; antidiasthmatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidialeratic; antidiantic; antidiammatory; conditions; antidiabetic; antidialeratic; antidiadetic; antidialeratic; antidiadetic; antidiadetic; antidiadetic; conditions; and antidiadetic; conditions and diagnosing pathological conditions. Polynucleotides and conditions and diagnosing pathological conditions. Polynucleotides, antibodies, agonists and antagonists from the present immune disorders by activating or invention may be used for treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune calls; to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the present
Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 TGAAATTTTACACAAAGCTAGATTTAGTTACATTCTTCCAATTTTGGGAA 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 10 other;
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Percent Identity: 99.815
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                                                                                                                         Claim 1; Page 751-752; 2352pp; English.
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1067 TCTAATAGAAAGTGGATGGGCACAAAATCCAGATGAAAGACCATCTTTCT
                                                                                                                                                                                                                                                                                                                                                                  AsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLe
                                                                                                                  217 lileThrTrpGluValLeuSerArgLysGlnProPheGluAspValThrA
                                                                                                                                                                                                                        ThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa
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                                                                                        AATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTTGGTTT
                                                                                                         uSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerA
                                                                                                                                           laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro
                                                                                                                                                                              GlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaVa
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CARD-3; caspase recruitment domain; CARD-4; regulation; detection. caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-47;
                                                                                                                                                                                                                                                                                                    1816
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                                                                  1817 TCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAATT 1866
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                                                                                                                                                                                                                                                                        uGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnL
                                                                                                                                                                                                                   hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
 allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
                                                    434 lyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGln
                                                                                                          MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs
                                                                                                                                                               pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
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98US-0019942.
98US-0099041.
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ID Z09246 standard; cDNA; 1931
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/product=
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06-FEB-1998;
17-JUN-1998;
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This invention describes the isolation of nover numan caspase.

This invention describes the isolation of nover numan caspase.

The invention are involved in the regulation of caspase activation.

The invention are involved in the regulation of caspase activation.

The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and prophylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of are suffering from a disorder associated with abnormal level or rate of are suffering from a disorder associated with abnormal level or rate of activity of a caspase. Diseases that may be treated include cancer complex, abnormal activity of the TWF receptor complex, or abnormal activity of the TWF receptor complex.

Complex, abnormal activity of the TWF receptor complex, or abnormal activity of the TWF receptor complex, or abnormal activity of the TWF receptor complex.

Complex, abnormal activity of the TWF receptor complex, or abnormal activity of the TWF receptor complex, or abnormal activity of the TWF receptor complex.

Complex, abnormal activity of the TWF receptor complex (e.g. farticiallary follacular lymphoma, carcinomas associated with mutations of infections, Alzheimer's disease, parkinson's disease, amyotrophic lateral sclinfections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclenosis, rethinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and such scline such of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD
                                                                                                                                                                                Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
                                                                                                                                                                                                                                                                                                               Example 2; Fig 1; 181pp; English
                                                                               WPI; 1999-494269/41.
P-PSDB; Y31140.
                                                                                                                                                                                                                                                                                                                                                                                     invention
                          Bertin J;
                                                                                                                                                                                                                                                      survival
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describes the isolation of novel human caspase

Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 other; Length: 540 Gaps: 0 Percent Identity: 99.630 Quality: 2817.00 Ratio: 5.226 Harity: 99.815 Percent Similarity alignment_scores

alignment_block: US-09-445-223-1 x Z09246

to: 1931 from: 1 Align seg 1/1 to: 209246

214 ATGAACGGGAGGCCATCTGCAGCGCCCTGCCCACCATCCCTACCACAA 263 1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLy

34

314 CCGCCCCCCCACGCAGGCTGCCGTCCAGGTGCCCGTGAAGCACCTGCAC 363 67 eralaargHisAlaaspTrpargValGlnValAlaValLySHisLeuHis IleHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAl 21

34

364 ATCCACACTCCGCTGCTCGACAGTGAAGGAAGGATGTCTTAAGAGAAGC 413 aGluIleLeuHisLysAlaArgPheSerTyrIlePheProIleLeuGlyI 84

leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100 84

334 snIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGln 350 ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThr11eSerGly 400 284 euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300 367 oGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetL 384 563 613 663 167 AATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTTGGTTT 713 uSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerA 184 laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro 200 813 217 AsnGluGluSerLeuProTyrAspIleProHisArgAlaArgMetIleSe 267 rLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL 284 134 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 301 ThrPheteuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT yrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGln AsnileLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLe GlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaVa 217 lileThrTrpGluValLeuSerArgLysGlnProPheGluAspValThrA GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl 351 384 564 267 117 134 614 151 664 167 714 184 764 201

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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-8; CIDE-8; CIDE-8; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compositions for identifying apoptosis signalling pathway inhibitors
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                                                                                                                   1464 AATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTG 1513
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                            SerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerAl
                                                                                      allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
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                                                                                                                                                                                                                                                                                                                                  hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
                                                          1414 TCTCAAAGGGCTGCATTCTGTGATCACAAGACCATTCCATGCTCTTCAGC
                                                                                                                                                 434 lyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human RICK coding sequence.
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This sequence encodes the number with fire interacting the invention. The RICK protein acts as a positive requiator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 caring CDPS signalling pathway inhibitors and activators, and methods and apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK, in the interactions of disease associated with excess cell growth and dysrequiation of apoptosis. Complexes containing RICK and CLARP can be used in drug creening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overspression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

Clentification of ARC-11ke inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, can be used as reagents for the preparation or affinity chromatography complexed and confidentially measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such ass CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular grows appropriate and capital drug candidates.
                                                                                           sequence encodes the human RICK (RIP-like interacting CLARP kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 IleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAs 100
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Percent Identity: 99.445
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                                        Claim 8; Fig 7b; 93pp; English.
for treating diseases
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Ratio: 5.200
Percent Similarity: 99.815
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US-09-445-223-1 x 248762
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                                                                                                                                                                                                                                                                                                                                                                                                      erLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPhe
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                                                                                                                                                                                                                                                                               LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl
                                                                                      150 nAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyL
                                                                                                    675 GAATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTGGTT
                                                                                                                                              euSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSer
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                                                                                                                                                                                                                                                                                                                                           AsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGl
575 CTTGGCCATTGAGATTTCGCATCCTGCATGAAATTGCCCTTGGTGTAAAT
                             134 TyrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGl
                                           725 TATCAAAGIGGCGCAIGAIGICCCICICACAGICACGAAGIAGCAAAICI
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New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; addison's disease; allergy; autoimmune hemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colltis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human breast and ovarian cancer associated antigen gene SEQ ID 228.
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                            1525 GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCA
                                                                            ACTIGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGG
                                                                                                                                                                                               1675 ACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGA
                                                                                                                                                                                                                                             uPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyL
                                                                                                                                                                                                                                                             euGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn
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                                                                                                                                                                               ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGl
                                                            nMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgA
GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGl
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ID F21841 standard; DNA; 463
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Dreast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antifinfammatory; antiviral; anticonvulsant; antibacterial; antifinfammatory; antioner; valuerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynocleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crobn's cardiovascular disorders such as myocardial ischemmias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
Sequences F21614 - F22031 represent DNA sequences encoding human proteins
                          B58711 - B59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences F22032 - F22040 and B59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious diseases.
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Sequence 463 BP; 150 A; 92 C; 89 G; 131 T; 1 other;

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Percent Identity: 99.333
               Length:
                                                                                                               Align seg 1/1 to: F21841 from: 1 to: 463
            797.00
5.349
99.333
                                                                 alignment_block:
US-09-445-223-1 x F21841
               Quality:
                                      Percent Similarity:
                            Ratio
alignment_scores:
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52 97 TyrMetProAsnGlySerLeuAsnGluLeuLeuHisArgLysThrGluTy

113 rProAspValAlaTrpProLeuArgPheArgIleLeuHisGluIleAlaL 130

130 euGlyValAsnTyrLeuHisAsnMetThrProProLeuLeuHisHisAsp 146

103 TIGGIGIAAATTACCIGCACAATAIGACTCCTCCTTTACTTCATCATGAC 152

147 LeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAl 163 153 TTGAAGACTCAGAATATCTTATTGGACAATGAATTTCATGTTAAGATTGC

197

230 luAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGlyHis 246

403 AAGATGTCACCAATCCTTTGCAGATAATGTATAGTGTCACAAGGACAT 452

Gaps: 26 Percent Identity: 34.074

54.444 579.00 1.969

Percent Similarity:

Quality:

alignment_scores:

Ratio:

to: 2370

from: 1

to: 261161

Align seg 1/1

alignment_block: US-09-445-223-1 x Z61161

Length:

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:261161

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Z61161 standard; DNA; 2370 BP.
seq_documentation_block:
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The present sequence encodes a murine death associated kinase protein, containing ankyrin repeats, designated DAKAR. The DAKAR polynuclectides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. DAKAR polypeptides and fragmented polypeptides are used for purifying proteins, e.g. to measure protein activity; as quality assurance agents to monitor shelf life and stability of binding partner proteins; as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds which may interfere with apoptosis; as molecular weight and isoelectric focusing markers; as controls for peptide fragmentation; identification of unknown proteins, e.g. by comparison with proteins in databases; and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography. The antibodies can also be used to block binding of the DAMAR polypeptides to their binding partners. Compounds that inhibit the protein are negligible to the DAMAR can be used to the Leat diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAKAR) used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel death associated kinase containing ankyrin repeats (DAKAR) used
as molecular weight marker and as controls for peptide fragmentation
                                                                                                                      Death associated kinase protein containing ankyrin repeats; DAKAR; kinase; quality assurance agent; shelf life; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production or
                                                                                      DNA encoding a death associated kinase with ankyrin repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characterized by overproduction or upregulated
                                                                                                                                                                                                              Location/Qualifiers
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98US-0099973.
99US-0119353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP.
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11-SEP-1998;
09-FEB-1999;
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10 49 26	LeuProThrIleProTyrHisLysLeualaaspLeuArgTyrLeuSerar	26 98 43 148
	InValalaValLysHisLeuHisIleHisThrProLeuLeu ::: :: GGCTGGGATCAAGTGCTGGCCGGTCGAC	56 186
57	LeuHisLys. ::::: ATGGAGATG	73 236
73	aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP ::: :: ::	90 282
90	heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu ::: :: .::: GTGGGCTTGGTCATGGAGTACATGGAGACGCTCCCTGGAGAAGCTG	106 330
31	LeuHisargLysThrGluTyrProAspValalaTrpProLeuArgPhear	123 368
123 369	glleLeuHisGlulleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP ::: ::: :::	140 418
140 419	roproleuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 	156 468
157	GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe :::::: :::	173 518
173 519	tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyG	188 556 ·
188 557	nTyrGlu :::: AATTCGT	204
205 601	ArgalaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTr ::: :: ::: CGCTTGTTGACACCAAACATGATGTATACAGCTTCGCCATTGTGATCTG	220 650
220 651	pGluValLeuSerArgLysGlnPrOPheGluAspValThrAsnProLeuG	237 700
237 701	InileMetTyrSerValSerGlnGlyHisArgProvalileAsnGluGlu ::	253 738
254 739	AAr CAG	267 788
267	7 S	284 831
80 (euLysCysLeuIleGluLeuGluProV	300
301	ThrPheLeuGluAlaVallleGluLeuLvsLvsThrLvsLeuGluSerV	* ~

	111 847 ACC		849
	317 ISerSerAlaileH1 ::::: 850 .TCTGAACAGAGA	SLeuCysAspLysLysMetGluLeuSerLeuA 	334 894
	334 snIleProValAs ::: 895GACCTGGC	eProValAsnHisGlyProGlnGluGluSerCysGlySerSerGln 3 ::	350 939
	351 LeuHisGluAsnS ::: 940 AGTGAGGCCAGGC	LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 3 :: ::	367 989
	367 oGlnAspAsnAsp.PheLeuSer ::: 990 CTTCGATAACGACTGCAGTCTCT	ArgLysAlaGlnAspCysTyrPheMet::: ::: :::CGAGTTGC	383 1021
	384 LysLeuHisHisC 1022T	rileserGl .ACTCTGGG	400 1041
	400 ySerGlnargala 111 1042 ATCTCCCAGACTC	rThrProCysSerSerA ::: GGCCCCGAAGAGCTCAG	417 1076
	417 laIleIleAsnProLeuSer' ::: 1077 CCGAAGITCCTCTG		433
	434 GlyIleAlaGln. ::::: ::: 1112 GCAGTGGCAAGAG	GlnTrpTleGlnSerLysAr 	444 1161
	444 gGluAspileVal	gGluAspIleValAsnGlnMetThrGluAlaCyșLeuAsnGlnSerLeuA 4 ::: TCCAGAGGATCGCTGT	461 1178
	461 spalaLeuLeuSe ::: 1179 ACTGTCTTTTGAG	uAspTyrGluLeuVal	477 1192
	478 SerThrLysProT	SerLysValArgGlnLeuLeuAspThr ::: ::::: ggGAAGCTTCAACAGGCGACCTGGGCCCC	493 1221
	494 Thraspileging 		510 1271
	510 sAspAsnLysGlr::::::::::::::::::::::::::::::::::::	saspasnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS : :::::	527 1321
	527 erArgSerProSerLeu ::	SerLeu 532 AGCCTG 1338	•
sed	_name: /cgn1_8/gcgc	/cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:261784	
seq.	_documentation_block Z61784 standard; c	k: cDNa; 3516 BP.	
X X	261784;		
E X	27-MAR-2000 (first	Ψ	
X	cDNA encoding murine	protein kinase/ankyrin h	SEQ ID NO:25.
XXX	Skin; dermal papilla; ke embryonic skin cell; ker secreted: transmembrane:	ratinocyte; neonatal atinocyte stem cell; inflammation; cancer	foreskin fibroblast; transit amplifying cel. ; neurological disease

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73 aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate spithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences Z61606-Z61832 represent cDNA sequences derived from z61725-Z61765, Z61802-Z61811 and Z61826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences Z61650-Z61668, Z61810, Z61812-Z61817 and Z61827-Z61829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to novel nucleic acid sequences derived from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides useful for the treatment of various conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encode proteins with one or more putative transmembrane domains
angiogenesis; tumour vascularisation; growth disorder;
developmental disorder; skin wound; hair follicle disorder;
anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kumble A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 lnValAlaValLys......HisLeuHisIleHisThrProLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 540
Gaps: 26
Percent Identity: 34.074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 158-159; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Z61784 from: 1
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Quality:
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09-NOV-1998;
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181 27

AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl

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140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      733 CIGCCACCCATCIGCAGACCCCGGCCGCGTGCCTGTGCCAGCCTGAIAGG 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 snIleProvalAsnHisGlyProGlnGluGluSerCysGlySerSerGln 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 oGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly.....G 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 lyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLysSer 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 InIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluGlu 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 SerLeuProTyrAspIleProHisArg......AlaArgMetIleSe 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 lSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeuA 334
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                                                                                                                                                                                                                                                                              glleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP
                                                                                                                                                                                                                                                                                                        roProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 CACTACCATGTCAAGATTTCTGACTTTGGGCTGGCCAAGTGCAATGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934 AGIGAGGCCAGGCCCGAGICCTCACGCCTCAAGCGCGCCTCIGCTCCCCC
                                                 90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu
                                                                                                                                                                                                                   ....GACCTGGCTCATGAGCCAGGCGAGAAAAGCTCTCTAGAGTCCAAG
231 CAAGTTCCGATACATTCTACCTGTGTACGCCATATGCCAGGAACCT....
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Murison JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1266 CACCAGGCTGATGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTCTAG 1315
                                                                                                                                  .....AAGGCCCCGAAGAGCTCAG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1216 ACAGACATCCAGAAGAAGAAGCTAGTGGATGCCATCATATCAGGGGACAC 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumble KD,
            ..... 1015
                                                                                                                                                                                                              461 spAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuVal 477
                                             384 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 SerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAspThr 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 sAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2001.DAT:C99717
                                                                                                                                                                                                                                                                                                                                                   1156 TCCAGAG......GATCGCTGT......C
                                                                                                                 400 ySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA
                                                                                                                                                                              417 lallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro
                                                                                                                                                                                                                                                  GlylleAlaGln...........GlnTrpIleGlnSerLysAr
                                                                                                                                                                                                                                                                                1106 GCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTTTCC
                                                                                                                                                                                                                                                                                                               gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA
                                                                                 ACTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 ThraspileGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLy
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                                                                               .....CACAGTTGG.....
            .....ccaagrigc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skin cell cDNA, SEQ ID NO: 257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID C99717 standard; cDNA; 3516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0312283
984 CTTCGATAACGACTGCAGTCTCT
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                                                                                                                                                  1036 ATCTCCCAGACTCTTG...
                                                                                                                                                                                                                CCGAAGTT...CCTCTG
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The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                       New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 gileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 ceccacrecrecaccragaccreaaeccaeceaacarccrecreereca 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 gGlyAlaSerGlyThrValSerSerAlaArgH18AlaAspTrpArgValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 CIGCGCACCITCGACGCCGGCGAAITCGCAGGCTGGGAGAAGGTGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 GGCTCGCGATCAAGTGCTCGCCCAGTCTGCACGTCGAC.......
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 540
Gaps: 26
Percent Identity: 34.074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 3516
                                                                                                                                              Claim 1; Page 216-218; 352pp; English
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1.969
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US-09-445-223-1 x C99717
2001-007495/01
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                       P-PSDB; B55958
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-	7	spalaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuVal	461
	461	gG1uAsp11eVa1AsnG1nMetThrG1uAlaCysLeuAsnG1nSerLeuA 	444 156
•	1155		10
	444	4 GlyileAlaGlnGlnTrpIleGlnSerLysAr	43
	433	7 laileileAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 	417
	417	U ySerGinArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA 	400
	1035	TGT	016
	400	4 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl	38
	383 1015	7 oGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet	36
	367 983	<pre>1 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 1:: :: </pre>	93, 5
	3	:	88
	350	4 snIleProValAsnHisGlyProGlnGluGluGerCysGlySerSerGln	33
	334 888	/ ISSENSETALATIEHISLEUCYSASPLYSLYSLYSMEGGLULEUSETLEUA	31./ 844
	843	- 45	841
	317	Thr	301
	840	6	82(
	0	euLy	284
	284	7 rLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL : :::	267
•	267	4 SerLeuProTyrAspileProHisArgAlaArgMetileSe	73
	253	7 InlleMetTyrSerValSerGlnGlyHisArgProVallleAsnGluGlu::	23,
	237	0 pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG	22
	220	5 ArgalaSerIleLysHisAspIleTyrSerTyrAlaVal1IleThrTr 	20
	204	8 lyThrileileTyrMetProProGluAsnTyrGluProGlyGlnLysSer :::	18(
	188	3 tSerLeuSerGinSerArgSerSerLysSerAlaProGluGlyG	17

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The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences 261606-261832 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences 261606-261891 and 261826 encode proteins with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell. secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides useful for the treatment of various conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding murine RIP protein kinase homologue, SEQ ID NO:403.
                                                                                                                                            ......GGGAAGCTTCAACAGGCGACCTGGGCCCC 1215
                                                                                                                    494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLy 510
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                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:Z61830
                                        SerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAspThr
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                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID Z61830 standard; cDNA; 1774 BP.
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98US-0188930.
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1173 ACTGTCTTTTGAGC.
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                                                                             1187 .....
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09-NOV-1998;
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                                        478
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Length: 540 Gaps: 26 Percent Identity: 33.889 Style=LalaaspleuargTyrLeuserAr 26 Style=LalaaspleuargTyrLeuserAr 26 Style=LalaargHisAlaaspTrpargValG 43 Style=LalaargHisAlaaspTrpargValG 43 Style=LalaargHisAlaaspTrpargValG 43 Style=LalaargHisAlaaspTrpargValG 43 Style=LalaargHisAlaaspTrpargValG 43 Style=LalaargHisAlaaspTrpargValG 43 Style=LalaargHisTyrColeuleu 56 Style=LalaargHisTyrColeuleu 56 Style=LalaargHisTyrColeuleu 56 Style=LalaargHisTyrColeuleu 56 Style=LalaargHisTyrColeuleu 106 Style=LalaargHisTyrColeuargPhear 123 Style=LalaargHisTyrColeuargPhear 123 Style=LalaargHisTyrColeuargPhear 123 Style=LalaargHisTyrColeuargPhear 123 Style=LalaargHisTyrColeuargPhear 124 Style=LalaargHisTyrColeuargPhear 125 Style=LalaargHisTyrColeuargPhear 126 Style=LalaargHisTyrColeuargPhear 127 Style=LalaargHisTyrColeuargPhear 128 Style=LalaargHisTyrColeuargHisTyrColeuargPhear 128 Style=LalaargHisTyrColeu	Length: 540 Gaps: 26 ercent Identity: 33.889 sleunlaaspleuargTyrLeuserAr 26 sleunlaaspleuargTyrLeuserAr 26 sleilli:::::::::::::::::::::::::::::::::
CAT 26 CTC 94 CTC 94 CTC 94 CTC 94 CTC 94 CTC 94 CTC 93 CGC 23 CGC 11 CTG 36 CTC 91 CTG 36 CTC 41 CT	EAT 26 CTC 94 CTC 94 CEU 56 CTC 94 CEU 56 CEU 104 CEU 56 CEU 105 CEU 56 CEU 56 CEU 56 CEU 56 CEU 106 CEU 56 CEU 107 CE
CAR 26 CTC 94 alg 43 CGT 14 CGT 14 Leu 56 CTG 32 CTG 32 CTG 32 CTG 32 CTG 32 CTG 36 CTG 41 CTG 36 CTG 41	CAT 26 CTC 94 CTC 94 Sal 6 43 CGT 144 CGT 144 CGT 23 CGG 36 CGG 36 CGG 46 CG
EAR 26 CTC 94 31 CGT 14 CGT 12 CGT 14 CGT 15 CGT 11 CGT 15 CGT 15 CGT 15 CGT 15 CGT 15 CGT 15 CGT 16 CGT 16 CGT 17 CGT 17 CGT 18 CGT 17 CGT 18	EAR 26 CTC 14 CTC 94 alg 43 alg 53 al
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Thrproleuleu 56 Thrproleuleu 56 Thrproleuleu 18 Thrproleuleu 17 Thriff	ThrproLeuLeu 56
1 1 1 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	C C C C C C C C C C C C C C C C C C C
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3 3 6 3 3 6 3 3 6 3 3 6 3 3 6 3 3 6 3 6	21
P 14 C 41 C 46 C 46 C 17 E 17 F 51 F 51 F 55	141 141 141 141 141 151 151 151 151 151
15 46 17 51 18 55	15 46 17 17 51 18 20 20 59
17 51 18 55	17 51 18 55 20 59
G 18 G 55	18 55 20 59
	20
ArgalaSerileLysHisAspileTyrSerTyralaValileThrTr 220 	

237	InllemetTyrSerValSerGlnGlyHisArgProValIleAsnGluGlu :: :: :::	253 734
254	eProHisArghlaAr ::: accccgcccccrcrcrcAcA	267.
267	rLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL ::::::::	284
284		300
301	hrPheLeuGluAlaValIleGlnLeuLysLysTh 	317
. .	CSETALAILEHISLEUCYSASPLYSLYSLYSWEtGluLeuSerLeu ::::: ::: CSAAACAGAAGACCTTTGTGAGAAGCCTGATGAGGAGGTGAAA	334
334	snlleProValAsnHisGlyProGlnGluGluGerCysGlySerSerGln :::	350 935
351 936	euHisGluA ::: GTGAGGCCA	367 985
367 986	OGINASPASNASP.PheLeuSerArgLysAlaGINASpCysTyrPheMet	383 1017
384	SerTrpAspSerThrIle AGTTGGACT	400
400	erGlnArgAlaAlaPheCysA 	417
417	rThrAlaGly	433
434	GGGGGT	444
1158	gGluaspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA ::: TCCAGAGGATCGCTGT	461
461	1LeuSerArgAspLeuIl TTGAGC	477
478	rgThrSerLysValArgGlnLeuLeuA. 	493
494	/G1 3AA	510 1267
510	SASPASDLYSGINMEtGlyLeuGInProTyrProGluIJeLeuValValS::::: :::	527

527 erArgSerProSerLeu 532

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43 lnValAlaValLys.........HisLeuHisIleHisThrProLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
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                                                                                                                                                                                                                                                                                                                                                               nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kumble KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
                                                                  seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2001.DAT:C99763
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Percent Identity: 33.889
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                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                       Skin cell cDNA, SEQ ID NO: 403
                                                                                                                   seq_documentation_block:
ID C99763 standard; cDNA; 1774
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08-MAR-2001 (first entry)
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US-09-445-223-1 x C99763
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P-PSDB; B56062.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200069884-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
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326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 GGGTGTGCTTACACAGAAGAAGCCATTTGCAGATGAAAAGAACATCCTAC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 InIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluGlu 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .TCTGAAACAGAAGACCTTTGTGAGAAGCCTGATGAGGAGGTGAA.... 890
                                                                        73
                                                                                                                              183 GACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGC
                                                                                                                                                                                73 aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP
                                                                                                                                                                                                               heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu
                                                                                                                                                                                                                                                                                                                       327 CTGGCCTCAGAG......CCATTGCCTTGGGACCTGCGCTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 gIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 CATCGTGCACGAGACAGCCGTGGCATGAACTTCCTGCATTGCATGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 CACTACCATGTCAAGATTTCTGACTTTGGGCTGGCCAAGTGCAATGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly.....G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GICCCACTCTCATGACCTCAGCATG......GATGGCCTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 lyThrileIleTyrMetProProGluAsnTyrGluProGlyGlnLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 CGCTTGTTTGACACCAACATGTGTATACAGCTTCGCCATTGTGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 SerLeuProTyrAspIleProHisArg......AlaArgMetIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1 :::|||1:::
735 CTGCCCACCCATCTGCAGACCCCGGCCGTGCCTGTGCCAGCCTGATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 rLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....ACCITCCAAGAAATI
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                                                                                                                                                                                                                                                                                                                                                                                                LeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      785 GATAATGCAACGGTGCTGGCATGCAGACCCACAGGTGCGGCCC.....
                                                                           AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl
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145 GGCTCGCGAGTCAAGTGCTCGCCCAGTCTGCACGTCGAC...
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17-FEB-2000

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1188
                                                                                                                                                                                                                                                                                                                                        1038 ATCTCCCAGACTCTTG........AAGGCCCCGAAGAGCTCAG 1072
                                                                                                                                                                                                                                                                                                                                                                                                        CCGAAGIT...CCTCTG......AATGCAAGTTCCCATCGTCCA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1218 ACAGACATCCAGAAGAAGAAGCTAGTGGATGCCATCATATCAGGGGACAC 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1268 CAGCAGGCTGATGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTCTAG 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTTTCC 1157
                                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                                                                                                417 laileileAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 spAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuVal 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 sAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS 527
334 snileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGln 350
                                                                                                                                                 oGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 SerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAspThr 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:258584
                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 GlyIleAlaGln......GlnTrpIleGlnSerLysAr
                               ....GACCTGGCTCATGAGCCAGGCGAGAAAGCTCTCTAGAGTCCAAG
                                                                                             LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl
                                                                                                                                                                                                                                                                1018 ......rgr....cacagrrgg.....acrcrggg
                                                                                                                                                                                                                                                                                                        400 ySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLy
                                                                       351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fel; protein kinase; mouse; signal transduction; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1158 TCCAGAG.....GATCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 3..2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID 258584 standard; cDNA; 2294 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse protein kinase Fel cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1318 ACAGCAGTGCCAGCCTG 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erArgSerProSerLeu 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200008178-A2
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                                   891
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The present sequence is that of Genesis clone 971025TRAM004820HT

(Fel) DNA. The translation of the clone (frame 3) is provided in

(T79154. The prolypeptide has kinase activity. The invention
relates to purified murine polypeptides (see Y79152-56) that
have kinase function and isolated nucleic acids encoding them (see
CN 25882-86). The nucleic acids can be used to express the
polypeptides, as probes to identify nucleic acids encoding proteins
polypeptides, as probes to identify nucleic acids encoding proteins
having kinase activity, and in assays to identify chromosomes; map
nucleic acids and bott unmours. Vectors comprising the novel
nucleic acids and host cells (bacterial, yeast, plant, insect or
animal) transfected or transduced with the vectors are claimed.
The kinase polypeptides and their fragments are used as mol.wt. and
isoelectric focusing markers, and as controls for peptide
fragmentation. They also have a number of therapeutic uses, as
kinases play a central role in cellular signal transduction.
                                                                                                                                                                                                                                                         Novel murine polynucleotides encoding kinase polypeptides, used a probes to identify nucleic acids encoding proteins having kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 resecreases......ccarrecerreseacerecerrese 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeuL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 spSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValGl 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GGCGCCTTCGGGCAGGTGTACAAGGTGCCCATGTGCACTGGAAGACGTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2294 BP; 526 A; 639 C; 666 G; 463 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 523
Gaps: 26
Percent Identity: 34.608
                                                                                                                                                                 Anderson DM, 'Marken JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 .to: Z58584 from: 1 to: 2294
                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3; 93pp; English
                                                                      98US-0095269
98US-0099973
                                   99WO-US17577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              577.00
2.025
54.493
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                                                                                                                             (IMMV ) IMMUNEX CORP
                                                                                                                                                                   Virca GD, Bird TA,
                                                                                                                                                                                                        WPI; 2000-205722/18
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                                                                                                                                                                                                                           P-PSDB; Y79154
                                   04-AUG-1999;
                                                                    04-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
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                                                                                                                                                                                                                                                                                                  activity
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4 8 8 8 6 2 2 7 8 2 5 9 9 8 8 7 1 7 7	94 ACTACCATCTCAAGATTTCTGACTTTGGGCTGGCCAAGTGCAATGGCATG 75 SCT. CAACCATGTCAAGATTTCTGACTTTGGGCTGGCCCAAGTGCAATGGCATGGCATG 76 SCT. CAACCATGTCAAGATTTCTGACTTTGGGCTGGCCCAAGTGCCTGTTTGG 77 TCCCACTCTCATGACCTCAGCATG
34 118 51 64 67 67 00 66 17	AlaileHisLeuCysAsplysLysMetGluLeuSerLeuAs 3 AcAGAGACTTTGTGAGAGCCTGATGAGGAGGTGAAA 8 AvalasnHisGlyProGlnGluGluSerCysGlySerSerGlnL 3 Sister
34	erThrAlaGlyAsnSerGluArgLeuGlnProG 4

434 IyileAlaGln 	<pre>LylleAlaGlnGlnTrplleGlnSerLysArg 444 ::::: ::: </pre>
445 GluAspIleValAsr ::: 1087 CCAGAG	GluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAs 461 ::: CCAGAG.
pAlaLe ::: CTGTCT	478
478 erThrLysProThrA	erThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrT 494 ::: ::: GGGAAGCTTCAACAGGCGACCTGGGCCCA 1146
494 hraspileginglyG : 1147 CAGACATCCAGAAGF	hraspileginglyglugluphealalysvalilevalginlysleulys 510 :::::::::: ::: ::::: CAGACATCCAGAAGAAGGTAGTGGATGCCATCATATCAGGGGACACC 1196
511 AspasnLysGlnMet ::::: 1197 AGCAGGCTGATGAAG	AspasnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSe 527 :::::: :::
527 rargSerProSerLeu 532 : 1247 CAGCAGTGCCAGCCTG 1262	arLeu 532 SCCTG 1262
seq_name: /cgn1_8/gcgdat	_name: /cgn1_8/gcgdata/geneseq/geneseqn/NN2000.DAT:261671
seq_documentation_block: ID Z61671 standard; cDNA;	ock: ; cDna; 1888 BP.
AC Z61671;	
DT 27-MAR-2000 (first	irst entry)
DE CDNA encoding murine RIP	urine RIP protein kinase homologue, SEQ ID NO:66.
	pilla; keratinocyte; neonatal foreskin fibroblast; cell; keratinocyte stem cell; transit amplifying cell;
	<pre>Secteted; transmemorane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.</pre>
XX OS Mus sp.	
XX PN W09955865-A1.	
PD 04-NOV-1999.	
29-APR-1999;	99WO-NZ00051.
29-APR-1998; 98US 09-NOV-1998; 98US	98US-0069726. 98US-0188930.
PA (GENE-) GENESIS RES	RES & DEV CORP LTD.
PI Strachan L, Sleeman	eeman M, Watson JD, Onrust R, Kumble A, Murison JG;
DR WPI; 2000-072177/06 DR P-PSDB; Y76007.	7/06.
PT Novel polynucleotides PT including wounds and o	otides useful for the treatment of various conditions and cancer -
PS Claim 1; Page 85-86; XX	5-86; 235pp; English.
CC The invention relates	slates to novel nucleic acid sequences derived from rat

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and mouse embryonic skin, kerathocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of kerathocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences 261605-261812 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences 261606-261849, 261725-261765, 261802-261811 and 261826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences 261650-261668, 261766-261780, 261812-261817 and 261812-261819 encode proteins with one or more putative transmembrane domains.
neonatal foreskin fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1888 BP; 433 A; 518 C; 554 G; 380 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 541
Gaps: 27
Percent Identity: 33.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 1888
     and
dermal papilla, human keratinocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548.00
1.845
54.898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: 261671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-445-223-1 x Z61671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
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CTGGCCTCAGAG......CCATTGCCTTGGGACCTGCGCTTTCG 362 230 LeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheAr 123 glleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140 463 CACTACCAAATGTCAAGATTTCTTGACTTTGGGCTGGCCAAGTGCAATGG 512 172 tMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly.... 187 90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu 106 324 363 CATCGTGCACGAGACAGCCGTGGGCATGAACTTCCTGCATTGCATGTCTC 412 roProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 156 CGCCACTGCTCCACATGAGCCAGCGAACATCTTGCTGGATGCC 462 GluPheHisVal...LysIleAlaAspPheGlyLeuSerLysTrpArgMe 172 73 56 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG 43 43 CTGCGCACCTTCGACGCCGGCGAATTCGCAGGCTGGGAGAAGGTGGGCTC 92 10 LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 43 InValAlaValLys........HisLeuHisIleHisThrProLeuLeu 73 aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP 57 AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl

56

277

325

107

123

88. GITTHITTELET STATE PROGUENTS THE PROGUENT GITTHITTELET STATE S	492	sValArgGlı	47.
10	19	:::	17
11		euAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLe	9
108GlyPhileIleTrimetroProclausarTyclubrodlyGlnLys 203 17 TTGGTACAATCGCCTACCTCCTGGAGGAATTCGTGaGAGG 594 204 SerArgalaSerIleLySHiSASpileTyrSerTyrAlavalileth 219 17 TTGGTACAATCGCCTACCTCCTCCTGGAATTCGTGaGAGG 594 219 TTGGTACAATCGCTACCTCCTCCTCGGAATTCGTGaGAGG 594 219 TTTGGLUVALLeuSerArglySGlnProPheGluAspV1ThrAsnProL 236 210 TTTGGLUVALLeuSerArglySGlnProPheGluAspV1ThrAsnProL 236 211 GLILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	\vdash	::: TCCTCCAGAGGATCGCTGT	15
10	œ.	sArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSer	4
108GlyThileIleTyTweeProFoclusharTyTclubrodlyGlnLys 203 204 SerArgalaSerIleLySHiSASpileTyTsErTyTalavalileTh 219 205 SecAccTCCTCCTCCTCCTCGGGGATTCGTGGGAG 594 206 SerArgalaSerIleLySHiSASpileTyTsErTyTalavalileTh 219 219 TTGGTACAATCGCTACCTCCTCCTCGGGATTCGTGGGAG 594 219 TTGGTACAATCGACAATGAAGTGATACAGCTTCCCCCAATGGTGAT 645 219 TTTSCIUVALLEUSEAATGTACAAGTGTACAGCTTCCCCCAATGGTGAT 645 219 TTTSCIUVALLEUSEAATGTACAAGTGTACAAGTGTACAAGAACATCC 694 210 TTTSCIUVALLEUSEAATGTACAAGAATGTACAAGAACATCC 694 211	15	:::::: ::: CCAGCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCT	10
10	4	ProGly1leAlaGlnGlnTrpIleGlnSer	3
188 .GlyThTILETLETPETPAREPORDEGLUASNITYGLUPPCGLYGLUPyS 203 551 TTGCTACAATCGCTACCTCCCAGAGCGAATTGT.::::::::::::::::::::::::::::::::	, ,	CAGCCGAAGTTCCTCTGAATGCAAGCTCCCATCG	07
188 .GlyThTILETIETIETYMETPCPAGGGGLUSSNTYGGLUPPCGLYGIDLyS 203 551 TTGGTACAATCGCTACCTCCCAGGCGAATTCGTGAGAAG 594 204 SERAGAATCGCTACCTCCCTCCAGGCGAATTCGTGAGAAG 594 205 SETATGALASENTIELYSHISASPILETYTSETYTALAVAILETT 119 111 111	432	AICIICCCAA	2 4
188GlyThTILLELOFTYNEEPPPPCOLUANTYTGIUPFOGLYGILLys 203 11 11 11 11 11 11 11 1	416	rGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSe :::: 	39
88 .GlyThrilelleTyTwhetProProGludanTyrGluDroGlyGlnLys 20; 11	103	TGTACTCTG	01
88 .GlyThrileileTyrMetProProGluAsnTyrGluProGlyGlnLys 20; 51 TTGGTACAATCGCCTCCCCCAGAGCGAATTCCTGAGAG 59 64 SetArgalaSerileLysHisAspileTyrSerTyrAlavailleTh 21; 65 TTGGTACATCGCCCACAGCGAATTCCTGAGAG 59 64 SetArgalaSerileLysHisAspileTyrSerTyrAlavailleTh 21; 65 AGCCGCTTGTTGACACAACATGATGTATACAGCTTCGCCATTGTGAT 64 65 AGCCGCTTGTTTGACACAACATGATGTATACAGCTTCGCCATTGTGAT 64 66 CTGCGCTTGTTGACACAACATGATGTATACAGTTCCAGTTGAT 64 67 CTGGGGTTGTTTGACACAGAATAATCATTGCAGTTGAAAGACATCC 69 86 CTGGGGTTGTTACACAGAATAATCATTGCAGTTGAAAGACATCC 69 87 EACACATCATGATGAAAGTGGTAAAGGCCACCGCCCA	6	MetLysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrileS	00
88 .GJyThrIlelleTyMetProProGluAsnTyrGluProGlyGlnLys 20; 1		aProGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrP CCCCTTCGATAACGACTGCAGTCTCTCCGAGTTGC	ذہ ف
88 .GlyThrilelleTyrMetProProGludsnTyrGlubroGlyGlnLys 20;	00		r.
88 .GJyThrIlelleTyMetEroProGluAsnTyrGluProGlyGlnLys 20: 1	Ū.	GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProA	Š
88 .GJyThrilelleTyMetProProGluAsnTyrGluProGlyGlnLys 20: 1	4 6	euAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerS ::: ::: ::: SACCTGGCTCATGAGCCAGGCGAGAAAAGCTCTCTAGAGT	m 0
	6		٠ 4
88 .GlyThrilelleTyMetProProGludsnTyrGluproGlyGlnLyg 20; 1	4	ATTACC	4
88 .GJyThrilelleTyMetEroProGluAsnTyrGluProGlyGlnLys 20: 1	Ä	IleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnS	Õ
88GlyThrilelleTyrMetProProGludsnTyrGluproGlyGlnLys 20	4		(1)
88 .GlyThrileileTyrMetProFioGluAsnTyrGluProGlyGlnLys 20 1	ŏ	heLenLysCysLenTleGluLeuGluProValLeuArgThrPheGlu	œ
88GlyThrilelleTyrMetProProGludsnTyrGlubroGlyGlnLys 20	6 0	SestreullestusertyTrpAlacinAshroAsptunkgrtooser	o o
88GlyThrilelleTyrMetProFloGluAsnTyrGluProGlyGlnLys 20 1	Ò		, (
88 .GlyThrileileTyrMetProGluAsnTyrGluProGlyGlnLys 20	266	GluserLeuProTyrAspIleProHisArgAlaArgMet	io m
88GlyThrileileTyrMetProFioGluAsnTyrGluProGlyGlnLys 20	732	GUGLILLEMECTYFSETVALSETGINGLYHISATGFICVALLIEASNGL ::: :::	יס סי
88GlyThrileileTyrMetProProGluAsnTyrGluProGlyGlnLys 20			
88GlyThrileileTyrMetProProGluAsnTyrGluProGlyGlnLys 20 [1][1][1][1][1][1][1][1][1][1][1][1][1][ന് ത്	rTrpGluValLeuSerArgLysGlnProPheGluAspValThrAsnPro CTGGGGTGTGCTTACACAGAATAATCCATTTGCAGATGAAAAACATC	4
88GlyThrileileTyrMetProProGluAsnTyrGluProGlyGlnLys 20			on on
88GlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLys 20		TIGGIACAAITGGGTACICCTICCAAGAGGGAATTGGIGAG	n c
	0 0	GlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLy	ο i

to: 1888

from: 1

to: C99604

13

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43 CTGCGCACCTTCGACGCCGGCGAATTCGCAGGCTGGGAGAAGGTGGGCTC 92
                                                                                                                                                                   10 LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr
alignment_block:
US-09-445-223-1 x C99604
                                                                                                     Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murison JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; mootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
                                                                                                                                                                                                                                                                     1269 CACCAGCAGGCTGATGAAGATCTACAGCCCCAAGATGTGGACTTGGTTC 1318
                               KD,
                                                                                                                                    seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2001.DAT:C99604
                                                                                                                                                                                                                           509 uLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValV
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                                                                                              493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sleeman M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID C99604 standard; cDNA; 1888 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skin cell cDNA, SEQ ID NO: 66
                                                                                                                                                                                                                                                                                                                                                                                                                              1319 TAGACAGCAGTGCCAGCCTG 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-007495/01.
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Length: 541 Gaps: 27 Percent Identity: 33.272

548.00 1.845 54.898

Quality:

alignment_scores:

Ratio: Percent Similarity:

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362
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                 181 GACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGC 230
                                                                                                                                                                                                                                                                                                  90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu 106
                                                                                                                                                                                                                                                                                                                                      324
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                                                                                                                                                 73
43
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..GTCGGCTTGGTCATGGAGTACATGGAGAACAGGCTCCCTGGAGAAGCTG
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26 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG
                                                                     43 lnValAlaValLys.......HisLeuHisIleHisThrProLeuLeu
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                                                                                                                                                 57 AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl
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Mouse receptor interacting protein gene

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283 heLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGlu
                                               .....ACCTTCCAAGAA
                                                                                                                                                                                                                                                                                                                                 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLe
                                                                                               300 IleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSe
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                                                                                                                                                                                                                                                                                                    333 euAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSer
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                                                                                                                                                                                                                                                 847 ....TCTGAAACAGAAGACCTTTGTGAGAAGCCTGATGAGGAGGTGAAA.
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ID T43752 standard; cDNA; 2268
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                                                                                                                                               841 ATTACC
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(first entry)

13-FEB-1997

T43752

CXXXEX

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- useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A cDNA clone (T43752) codes for mouse receptor interacting protein (RIP) (W04627), a protein which contains a C-terminal death domain through which RIP interacts with the Fas/APO-1 intracellular domain (ICD). RIP overexpression leads to cell death. The RIP cDNA was identified from a mouse thymus cDNA library by screening with the human RIP coding sequence (see also T43753) and sequence analysis of overlapping clones. It can be used as a probe and to produce recombinant RIP in host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor interacting protein having death and kinase domain to control diseases that involve abnormal apoptosis, and for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||::: ||||::: ||| ||||||| ::: |||| ::: |||| CTAGACAGCGGAGGCTTCGGGAAGGTGTCCTTGTGTTACCACAGAAGCCA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 IGGATTIGICATCCIGAAAAA......GTATACACAGGGCCCAACC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 GCGCTGAGTACAATGAGGTTCTCTTGGAAGAGGGGAAGATGATGCACAGA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 spSerGluArgLysAspVal...LeuArgGluAlaGluIleLeuHisLys 72
                             Receptor interacting protein; RIP; cell death; apoptosis; Fas; APO-1; signal transduction; cancer; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 pargvalGlnValAlaValLySHisLeuHisIleHisThrProLeuLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2268 BP; 719 A; 491 C; 576 G; 482 T; 0 other;
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Gaps; 25
Percent Identity: 25.452
                                                                                                                                                                                                                                                                                                                                                                Stranger BZ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 38-39; 64pp; English.
                                                                                                             Location/Qualifiers
52..2022
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US-09-445-223-1 x T43752
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Percent Similarity:
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                                                                                 Mus sp.
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                                                                                                               Key
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309	GAACTATTCGCTGGTGATGGAGTACATGGAGAAGGGCAACCTGATGCACG	358
106 359	euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe::	122
123 400	ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh ::: :::	139 444
139 445	<pre>rProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspA :::::: </pre>	156 493
156 494	<pre>snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet ::::: ::: </pre>	172 543
173 544	MetSerLeuSerGlnSerArgSerSerLysSerAlaPro 	185 593
186 594		196 643
197 644	ACCTGAATGACATGCAAGGAAGTCG	208 681
209 682	LysHisAspIleTyrSerTyrAlaValIleThrTrpGluV ::: ::: : GACGTGTACAGCTTTGGCATTGTCCTTTGGGCAA	225 725
225 726	<pre>gLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerV : ::: ::: aAAGGAGCCCTATGAGAATGTCATCTGTACTGAGCAGTTCGTGATCTGCA</pre>	242 . 775
242 776	alSerGlnGlyHisArgProValIleAsnGluGluSerLeuPro :::::: :::	256 825
257 826	TyraspileProHisArgAlaArgMetileSerLeuileGluSerGlyTr::	273 857
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290 908	euGluProValLeuArgThrPheGluGluIleThrPheLeuGluAla ::::	305 954
306 955		316 1004
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353 155	uAsnSerGlySerProGluThr	360 1204

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361	rLeuProAlaProGlnA	370
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371	SpC	387
1255	GAGGCTTACAACAGAGGAGGAGAAAGGAAACGAAGGGTCTCTCA	1298
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432	lnProGly1leAlaGlnGlnTrpIleGlnSerLys	443
1490		1539
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1640	TIGGAAACCACAATTATATGGATG	1689
468		485
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485		499
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200	GluPheAlaLysValIleValGl	207
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1840	ATCGATGAAATCGACCATGACTATG 1864	

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/clone=Lib="NHHMGC.89"
/tissue_type="hypernephroma, cell line"
/tissue_t
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I (bases 1 to 811)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                        BG170405 811 bp mRNA EST 06-FEB-2001 602322736F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4426016 5', mRNA sequence.
BG170405 GI:12677108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnh.gov
Plate: LLAM10172 row: g column: 09
High quality sequence stop: 721.
Location/Qualifiers
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Gaps: 3
Percent Identity: 94.074
      337
446
400
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   1.5e-48
2.4e-48
5.1e-48
8.2e-48
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Ratio: 4.933
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                                                                                                                                                                  seq_name: gb_est97:BG170405
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gb_est92:BF825562
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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KEYWORDS
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BF754627 QV3-CT0558-121000-377
                                                                                                                                                                                                                                               AA315575
                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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6e-71
4e-64
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source
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ORIGIN
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COMMENT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                 302
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                 342 inGluGluSerCysGlySerSerGinLeuHisGluAsnSerGlySerPro 358
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                                                                                                                                   HistysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAl
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LOCUS BE877822
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/tispued: ling; Vector: pCMV-SPORT6; Site_1: Not1;

                              Tel: (301) 496-1550
Tel: (301) 496-1550
Email: Robert Strausbergenih, gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9609 row: q column: 24
High quality sequence stop: 739.
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Percent Identity: 98.361
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Robert Strausberg, Ph.D.
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Ratio: 4.846
Percent Similarity: 98.770
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Homo sapiens
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 654)
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                                                                                                                                    337 ValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGl 353
                                                                                                                                                                                                                                                                                                                                           105 ATGATTTTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 GCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAA 254
                                                                                                                                                              5 GTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGA
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Percent Identity: 99.512
                                                                                                 to: 828
                                                                                                 from: 1
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                                                                                              to: BE875947
Percent Similarity: 99.512
                                   alignment_block:
US-09-445-223-1 x BE875947
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BE536247
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Site_2: Sall: Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tels: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9669 row: n column: 06
High quality sequence stop: 795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 828)
1 thtp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE875947 828 bp mRNA EST 20-OCT-2000 601486423F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888965 5'
                                                                                                                                  550
            482 hrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIleGln.Gl 498
                                                                                                                                                                                             yGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnM 515
                                                                                                                                                                                                                                                                            etGlyLeu..GlnProTyrProGluIleLeuValValSerArgSerProS
                                                                                          465 rArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLysProT
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BE875947
BE875947.1 GI:10324723
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163 c
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Ratio: 5.029
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 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5 kb. Library prepared by Life Technologies.
                          Mattonia institutes of heatth, mammatran state contacts. When the contacts is sobert Strausberg, Ph.D.
Contacts. Robert Strausberg, Ph.D.
Tals: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cONA Library Preparation: Life Technologies, Inc.
cONA Library Arrayed by: Incyte Genomics, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
cDNA Library Arrayed by: Constitution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM84125 row: o column: 08
High quality sequence stop: 650.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 sLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 LysThrLysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLy 327
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Percent Identity: 95.890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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Ratio: 4.807
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Percent Similarity: 96.804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-445-223-1 x BE536247
                                                                                                                                                                                                                                                                                                                                                                                                                                   214
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                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                  TITLE
JOURNAL
   AUTHORS
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                                                    COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

11 (bases 1 to 645)

12 (bissoe, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Hillier, L., Lennon, G., Becker, M., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Mortis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA160647 645 bp mRNA EST 16-DEC-1996 zq49c11.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:633044 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Stratagene hwr neuron (#937233)"
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/lab_host="solk (kanamycin resistant)"
/note="Vector: pBluescript SK; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally, Primer: Oligo dT.
                                                                                                                                                                                                                                             494 ThrAspileGlnGly.GluGluPheAlaLysValileValGlnLys.Leu 509
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                            ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLe
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LOCUS AA160647
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alignment_scores:

Sequencing Center information can be

Ph.D., Michael

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/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker: plasmid DNA from the
normalized library NI_CGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
SUBSGOB-986759, 1101192-1101959, and 1217928-1220615).
Subtraction bento Soares and M. Fatima Bonaldo. "
11 c 128 g 200 t
       Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 592)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                         Tissue Procurement: Michael J. Brownstein, M.D., Ph. Emmert-Buck, M.D., Ph.D. cDN Library Preparation: M. Bento Scares, Ph.D. cDN Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLy 376
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2317103"
/clone_lib="NCI_GGAP_Pr28"
                                                                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 459.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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US-09-445-223-1 x AI745575/rev
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Ratio: 5.193
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                      AUTHORS
                                                                                                                                       JOURNAL
                                                     REFERENCE
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                                                                                             TITLE
                                                                                                                                                                 COMMENT
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LOCUS AI745575 592 bp mRNA EST 17-DEC-1999
DEFINITION wc34f12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2317103 3'
similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ;, mRNA
                                                                                                                                                                                                  281
                                                                                                                                                                                                                                                                                                                                                                                                           102 TGATCTCTAATAGAAAGTGGATGGGCACAAAATCCAGATGAAAGACCA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerPheLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGl 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uGluIleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 lnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeu 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIl 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 TITATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCAT 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTCTTAAAATGTTTAATAGAACTTGAACCAGTTTTGAGAACATTTGA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTCAGCTCCATGAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 roAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyr 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etlleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgPro
                       Gaps: 2
Percent Identity: 92.891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnProGlyIleAlaGlnGlnTrpIleGlnSer 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              598 CAGCCT...GTATGCCCGCAGTGGATCCGAGCA 627
                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AI745575
AI745575.1 GI:5113863
995.00
4.901
96.209
                                                                                                                                                          Align seg 1/1 to: AA160647
                                                                                                                US-09-445-223-1 x AA160647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est24:AI745575
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    Quality:
                                              Percent Similarity:
                         Ratio:
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348

352

265

282 152 298 202 382

398

415

432

493

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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534 TGCCAGAATTTCGGCACGAGGAAAATAGTGGTTCTCTTAAAATTTCAAG
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AM$60501 647 bp mRNA EST 01-JUN-2000
DEFINITION EST372572 MAGE resequences, MAGF Homo sapiens CDNA, mRNA sequence.
ACCESSION AW$60501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colon tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a model of
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                                                                                                                                                                                 509
                                                                                                                                                                                                 192 CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTG 143
                                                                                                                                                                                                                                            526
                                                                                                                      493
                                                                                                                                      LeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLe 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessment of gene expression patterns in a model metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528
Fax: 301 838 0208
292 CTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACT
                                                                                                                      uValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspT
                                                                                                                                                                                 hrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 647
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Percent Identity: 92.857
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1. .647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW960501.1 GI:8150185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: johnq@tigr.org
Plate: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-445-223-1 x AW960501/rev
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4.930
94.898
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Percent Similarity:
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ORIGIN
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VERSION
KEYWORDS
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                                                             460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BES51615 636 bp mRNA EST 10-AUG-2000 7442906.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3221434 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ; mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 636)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                         428
                                                                                                                                                                                                                                                        385
                                                                                                                                                                                                                                                                                                                                                                   462
                                                                                                                                                                                                                                                                                                                                                                                                        285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
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                                                                                         412
                                 535
                                                                     379 ASPCYSTYrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAs 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 ACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                         584 GGTCCCTGCCAGCTCTCCAAGCCAATGATTTTTTTATCTAGAAAAGCTCAA
                                                                                                                                             pSerThrIleSerGlySerGlnArgAlaAlaPheCysAspH1sLysThrT
                                                                                                                                                                                                                                       uAspileValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspA
                                                                                                                                                                                                                                                                                                                                                                                                            334 AGACATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArg
                                                                                                                                                                                                                     hrProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSer
Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est75:BE551615
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LOCUS BE551615
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/db_xref="taxon:9606"
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/tissue_type="Pooled germ cell tumors"
/tab_host="NetLor: pT773D-Pac (Pharmacia) with a modified
polylinker; plasmid DNA from the normalized library
NOI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive phyridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 147592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaido. " subtraction by
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHis 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLe 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 sAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 hrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 98.343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-445-223-1 x BE551615/rev
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5.022
98.343
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                                                                                                                      FEATURES
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seq_documentation_block:
LOCUS AA161113 568 bp mRNA EST 09-MAR-1998
DEFINITION 2058405.51 Stratagene pancreas (#937208) Homo sapiens cDNA clone
INAGE:591081 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   376 sAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis. 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
to: 568
                                   526 lSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 540
                                            137 TICTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 2
Percent Identity: 95.628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:4622467"
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                                                                                                                                   AA161113.1 GI:1735349
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                                                                       seq_name: gb_est3:AA161113
                                                                                                                                                             Homo sapiens
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                                                                                                                                                      human.
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                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                 AUTHORS
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/sex="female"
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4.424
87.611
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     primer:
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Ratio:
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                                                                                                                                                                                                                                                                BASE
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J. (bases 1 to 762)

Blas Neto.E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Rogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.bx
This sequence was derived from the FAPESP/LICR Human Cancer Genome Troject. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=LLat2=IL-BT067-023.html st3=190199st4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
GGCTCAAGACTGTTATTTANGAAGCTGCATCACTGTCCTGGAAATCACC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 CACTACTGACATCCAAGGAGAATTTGCCAAAGTTATAGTACAAAAT 119
                              118 AAAAGGGAAGNCATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysL
                                                                                                     SLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaG
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                                                                                                                                                                                                                                             LysArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGln.S
                                                                                                                                                                                                                                                                                                                   erLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGlu
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                                                                                                                                                                          lyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSer
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est26:A1904799
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VERSION
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MEDLINE
218
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//dev_stage="Adult"
//note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
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from ORESTES PCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIleG 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oGlnGluGluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSer 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTATN 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 ArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAs 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 ArgLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 rValSerGlnGlyHisArgProValIleAsnGluGluSerLeuProTyrA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 762
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157 c 137 g
                                                                      /db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
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408

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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seq_documentation_block:

LOCUS AW085560 606 bp mRNA EST 09-MAR-2000

DEFINITION wy67c04.x1 Soares_NSF_F8_9W_OT_PA_F_S1 Homo sapiens cDNA clone
IMAGE:2553606 3' similar to TR:043353 043353 SERINE/THREONINE

KINASE RICK: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 yrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGln 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 lileThrTrp..GluValLeuSerArgLysGlnProPheGluAspValTh 233
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                                                                                                                                             276 CCGCCCGCCACGCAGACTGGCGCGTCCAGGTGGCCGTGAAGCACCTGCAC 325
                                                                                                                                                                                                                                                                                                                                                                                                       84 leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 ACCTGCACAATATGACTCCTCTTTACTTCATCATGACTTGAAGACTCAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 uSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerA 184
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                                                                                                                    erAlaArgHisAlaAspTrpArgValGlnValAlaValLysHisLeuHis, 50
                                                                                                                                                                                                                                                                                                           67 aGluIleLeuHisLysAlaArgPheSerTyrIlePheProIleLeuGlyI 84
                        SLeuAlaAspLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 ACTCGCCGACCTGCGCTACCTGAGCCGCGCGCCCTCTGGCACTGTGTCGT
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I (bases 1 to 917)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: ATCC/CTP/DPTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: image.llnl.gov

Plate: LLCM71 row: m column: 24

High quality sequence stop: 734.
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                                                                                                                      176 ATGAACGGGAGGCCATCTGCAGCGCCCTGCCCACCATCCCTACCACAA 225
spHisLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThr 424
                                                                                         425 AlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGl 441
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                        Length: 269
Gaps: 5
Percent Identity: 69.888
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BE274455
BE274455.1 GI:9149397
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US-09-445-223-1 x BE274455
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FEATURES

BASE COUNT

ORIGIN

520

167

117

67

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 484)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

G.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G.; Blake,J.A., Brandon,R.C., Man-Wal,C., Clayton,R.D.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

J.L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palanques,R.F., McDonald,J.L., Saudek,D.M., Shirley,R.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Fendy,D.-F., Ferrle,A., Fischer,C., Hastings,G.A., He,W.W.,

HU,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Shirley,S., Ollins,E.J.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Fuelds,C., Fraser,C.M. and

W.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.hfml)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_documentation_block:
LOCUS AA315575 484 bp mRNA EST 19-APR-1997
DEFINITION EST187344 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5'
356 cectagareccerrerecasesacrirearcarsaassassarrars 307
                                                                                                                                                                                                     475 uLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuA 492
                                                                                                                                                                                                                                   492 spThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLys 508
                                                                                                                                                                                                                                                                                                                                            206 TIGAAAGATAACAAACAAAIGGGICITICAGCCITACCCGGAAATACTIGI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                509 LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erLeuAspAlaLeuLeuSerArgAsp.LeuIleMetLysGluAspTyrGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA315575.1 GI:1967904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: THC188294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est5:AA315575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA315575
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AUTHORS
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KEYWORDS
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                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ncce="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and 8s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was pCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneins: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NBHSF pool 1: 145032-14735, 147720-148103, 148872-149255, 15002 - 150407, 131176-15237 Soares NBHR pool 1: 758280-766583, 772104-774407 Soares NBHPA pool 1: 758280-766583, 772104-774400. 70999 Subtraction by Bento Soares and M. Fatima Bonaldo. " 1 others
                                                                                                                                                                                                  NOTICGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Finis clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 885 Std Error: 0.00
Seq primer: -40UP from Glbco.
High quality sequence stop: 470.
Location/Qualifiers
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 606)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 GlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSe 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 rLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="TWAGE:2553606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AW085560 from: 1 to: 606
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Percent Identity: 98.795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
              AW085560.1 GI:6040712
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5.110
98.795
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                                                                                                     Homo sapiens
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AUTHORS
TITLE
              VERSION
KEYWORDS
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alignment_scores:
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ORIGIN
                 ORGANISM
                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                        REFERENCE
                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                       FEATURES
     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="ATCC (inhost):110668"
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/clone_lib="Colon carcinoma (HCC) cell line II"
/tissue_lip="Colon"
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/cell_line="KM12C"(HCC)-parental human colon carcinoma ;Dukes B2"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
109 c 101 g 136 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eValThrGluTyrMetProAsnGlySerLeuAsnGluLeuLeuHisArgL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 uHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisV 160
                                                                                                                                                                                                                                                                                                                                                                                                                              102 GAAAGGATGTCTTAAGAGAGCTGAAATTTTACACAAAAGCTAGATTTAGT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 alLysIleAlaAspPheGlyLeuSerLysTrpArgMetMetSerLeuSer 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrIlePheProIleLeuGlyIleCysAsnGluProGluPheLeuGlyIl 93
                                                                                                                                                                                                                                                                                                       202 AGTTACTGAATACATGCCAAATGGNTCATTAAATGAACTCCTACATAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 nValAlaValLySHisLeuHisIleHisThrProLeuLeuAspSerGluA
                                                                                                                                                                                                                                                                                                                                                                                                                 rgLysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSer
                                                                                                                                                                                                    Gaps: 1
Percent Identity: 98.137
                                                                                                                                                                                        Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 CAGTCACGAAGTAGCAAAATCTGCACCAGAA 482
                                                                                                                                                                                   820.00
5.157
98.758
                                                                                                                                                                                                                                                                              Align seg 1/1 to: AA315575
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US-09-445-223-1 x AA315575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est10:AA655189
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                                                                                                                                                                                                              Percent Similarity:
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                 9
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra M.Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Fax: 314 286 1810
Final: mousesetSt@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer:
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/dev_stage="13 day embryos"
/lab_host="Solr (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Nector: Primer:
/note="Organ: heart; Nector: Strength SK-; Strength SK-; Strength SK-; SK-; Strength SK-; SK-; Strength SK-; SK-; SK-; Strength SK-; SK-; Strength SK-; SK-; Strength SK-; SK-; Strength SK-; Streng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Stratagene mouse heart (#937316)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 LeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPh 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 TyrMetProProGluAsnTyrGluProGlyGlnLysSerArgAlaSerIl 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 TCTCTCAATCACGAAGTTACAAATCTGCACCCGAAGGAGGAACAATCATC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CTGCTTCATCATCATAAAGACTCAGAATATCTTGTTGGATAATGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 91.617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: -28ml3 rev1 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .503
/organism="Mus musculus"
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1211518"
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US-09-445-223-1 x AA655189
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Percent Similarity:
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13 CTTGCCAGATA 3
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1..510.

/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone_lib="gxi0173"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: Smal;
/note="Organ: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

""" a 108 c 128 g 147 t
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-ST0173-041099-011-e06&t3-1999-101-004&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW389<u>8</u>63 510 bp mRNA EST 04-FEB-2000
RC2-ST0173-041099-011-e06 ST0173 Homo sapiens CDNA, mRNA sequence.
AW389863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 510)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                         258 pileProHisArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaG 275
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202 GAAGCATGATATATACAGCTATGCAGTTATCATGTGGGAAGTGTTATCCA
                                                           242 ValSerGlnGlyHisArgProValIleAsnGluGluSerLeuProTyrAs
                                                                                                                                                452 CCAGTICTGAGAACATTIGAAGACATAACTITCCTTGAGGCTGTTATTCA
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LOCUS AW389863
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                 Gaps: 2
Percent Identity: 72.851
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US-09-445-223-1 x AW389863/rev
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Percent Identity: 99.630
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        /cgnl_7/ptodata/l/ina/5A_COMB.seq:US-08-306-691B-17 + /cgnl_7/ptodata/l/ina/5B_COMB.seq:US-08-356-806A-64 + /cgnl_7/ptodata/l/ina/5A_COMB.seq:US-08-328-4 + /cgnl_7/ptodata/l/ina/6A_COMB.seq:US-09-143-314-64 + /cgnl_7/ptodata/l/ina/6B_COMB.seq:US-09-143-314-64 + /cgnl_7/ptodata/l/ina/6B_COMB.seq:US-09-209-668-12 +
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SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPY
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
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FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REGISTRATION NUMBER: 37,283
REFRENCE/POCKET NUMBER: 07334/06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
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CORRESPONDENCE ADDRESS:

SADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09019942
Patent No. 6033855
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US-09-445-223-1 x US-09-019-942-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY: USA
ZIP: 02110-2804
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US-09-019-942-2
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2.3e-20 2
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9.6e-24
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Sequence 257, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1988-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PhealaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLe
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Mouse US-09-188-930-257
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1186		0 1
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383 1015	OGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet CTTCGATAACGACTCCTCCGAGTTGC	367
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APPLICANT: STREAM, LOTING
APPLICANT: STEACHAN, LOTING
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Ornust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.101181:
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
LENGTH: 1888
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US-09-188-930-66
GENERAL INFORMATION:
APPLICANT: Watson, James D.
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203 594	8GlyThrileileTyrMetProProGluAsnTyrGluProGlyv ::: ::: TTGGTACAATCGCTACCTCCAGAGCGAATTCGT	18
187 550	rArgSerSerLysSerAlaProGluGly	17:
512	// GlupheHisValLysileAlaAspPheelyLebsElysilpAryMe ::::::::::::::::::::::::::::::::::::	46

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rgGlnLeuLeuAsp 492 :	ProGluIleLeuValV 526 : GATGTGGACTTGGTTC 1318	:US-08-444-005-14		2	3100		Version #1.30 5		01		
477 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLenAsp 1193	509 uLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValV ::::: :::	TAGACAGCAGTGCCAGCCTG ''Cgn1_7/ptodata/1/in	<pre>seq_documentation_block: ; Sequence 14, Application US/08444005 ; Patent No. 5674734</pre>	hi ia B B-H-C C	OF SEQUENCES: 35 ONDENCE ADDRESS: SSEE: Fish & Richardson P.C. T: 225 Franklin Street, Suite	 ZIF: UZIIU-Z804 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	-DOS #1.0, 44,00	FILING DATE: CLASSIFICATION: 435 ATTONNEY AGENT INFORMATION:	NAME: CLAIK, FAUL 1. REGISTATION NUMBER: 30,164 REFERENCE/DOCKET NUMBER: 00383/026001 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070	. 25 E.	LENGTH: ZJOB Dase pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA

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123 ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 alSerGlnGlyHisArgProValIleAsnGlu.....GluSerLeuPro 256
                                                                                                                                                                                                                                                                                                    168 TGGATTTGTCATCCTGAAAAA......GTATACACAGGGCCCAACC 208
                                                                                                                                                                                                                                                                                                                                                                      209 GCGCTGAGTACAATGAGGTTCTCTTGGAAGAGGGGAAGATGATGCACAGA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 GAACTATTCGCTGGTGATGGAGTACATGGAGAAGGGCAACCTGATGCACG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 MetSer...LeuSerGlnSerArgSerSerLysSerAlaPro..... 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 LysHisAspileTyrSerTyrAlaValIleThrTrpGluValLeuSerAr 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 gLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              857
                                                                                                                                                                                                     257 TyrAspIleProHisArgAlaArgMetIleSerLeuIleGluSerGlyTr 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 pAlaGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGluL 290
                                                                                                                                                                       40
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                                                                                                                                                                                                                                                                                                                                                                                                                                      73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl 89
                                                                                                                                                                       24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr
                                                                                                                                                                                                                                                                                                                                               57 spSerGluArgLysAspVal...LeuArgGluAlaGluIleLeuHisLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::||| | |||||::
359 IGCTA.....AAGACCCAGATA...GATGTCCCACTTTCATTGAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 TGGAGCAAACTGACTAAGGAGAAAGACAACAAGAAGAAGAAGTGAGCAG
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Gaps: 25
Percent Identity: 25.452
                                                                                                                            from: 1 to: 2268
                                                                                                                            .gn seg 1/1 to: US-08-444-005-14
                                                             gnment_block:
-09-445-223-1 x US-08-444-005-14
Ratio: 1.272 rcent Similarity: 51.232
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.740 CACCACTAGTCTGACTGATGAACACCTGAACCCTATCAGGGAAAACCTGG 1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 CCAAGCCGCTCTGGTGACTAAATTCATGGAGAACGCCTCCTTGTCGGGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 eArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 hrProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAsp 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 CCCTTGGTGTCCATCGAGGAACTGGAGAACCAGGAGCTCGTCGGCAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGl
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                                         ....GluPheAlaLysValIleValGl
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                                                                                                                                                                                                                                        seq_documentation_block:
Sequence 2, Application US/09329418
Sequence 2, Application US/09329418
Sequence 2, Application US/09329418
GENERAL INFORMATION:
TOTILE OF INVENTION:
FILE REFERENCE: PHA.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 499
Gaps: 21
Percent Identity: 28.056
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                                                                                                                                                                     1840 ATCGATGAAATCGACCATGACTATG 1864
                                                                                                                           nLysLeuLysAspAsnLysGlnMet 515
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US-09-445-223-1 x US-09-329-418-2
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1.452
54.509
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CORGANISM: Homo Sapiens
US-09-329-418-2
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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accggtgetcetgcaccggacctcaagccatccaacgtcctgctggac 453	1253 GTCCTGGACCCCGAGGGAATCAGGGGGCTGAGAG
AsnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMe 172 ::: ::	
	426 GlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSe 442 :::
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	<pre>seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:US-09-329-418-1 seq_documentation_block:</pre>
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etTyrSerValSerGlnGlyHisArgProValIleAsnGluGluSer 254 ::: ::::: ::: ::: ACGAAGCAGTGTGCAACAGGCAGAACCGGCCTTCATTGGCTGAG 732	FILE REFERENCE: PHM.70536 ; CURRENT APPLICATION UNBER: US/09/329,418 ; CURRENT FILING DATE: 1999-06-11 ; NUMBER OF SEQ ID NOS: 39
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ulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheLeuL 285 :::::: ::::: ::: : AarGCAGCTCTGCTGGAGCAGTGAGCACAGACCCTCCTTCCAGG 832	; ORGANISM: Homo Sapiens US-09-329-418-1
ysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIleThr 301 :: :: :: ::: AATGCCTACCAAAAACTGATGAAGTCTTCCAGATGTGGAGAAC 876	alignment_scores: Quality: 392.50 Length: 501 Ratio: 1.443 Gaps: 22 Percent Similarity: 54.291 Percent Identity: 28.144
PheLeuGlualaValIleGlnLeuLysLysThrLysLeuGlnSerValSe 318 ::::: ::::	k: -1 x US-09-329-418-1
rSer.AlaIleHisLeuCysAspLysLysLysMetGlu 330 	<pre>g 1/1 to: US-09-329-418-1 from: 1 to: 1873 ProfhrileProfyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGI </pre>
LeuserLeuasnIleProvalas 338 :::::: :: AAATGGATGGCTTTAGGAGAACCATAGAAACCAGCACTCTCGTAATGAT 1026	CCCTTGGTGTCGACGAGGAGCTGGAGGAGCTCGGCGCAAAGG yalaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnV :::
n.HisGlyProGlnGluGluSerCysGlySerSerGln 350 GTCATGGTTCTGAGTGGCTAAACAAACTGAATCTAGAGGAGCCTCCCAG 1076	CGGGTTCGGCACAGTGTTCCGGGCGCAACATAGGAAGTGGGGGCTACGATG alAlaValLySHisLeuHisIleHisThrProLeuLeuAspSerGluArg
LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 367 	504 IGGCGGICAAGAICGIAAACTCG 520 61 LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 77 61 Ill - - - - - - - - - - - - -
oGlnaspasnaspPheLeuSerArgLysAla	IllePheProlleLeuGlylleCysAsnG
GCAGGCACATCTTCAGATTCGATGGCCCAACCTCCCAGACTCCAGAGAC 1202	INProGluPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeu
CysTyrPheMetLysLeuHisHisCysPro	AsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLe
SSerTrpAspSerThrI1eSerGlySerGlnArgAlaAlaPheCysAspH 409 	uArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisA

1364 AGAGACCTCAACTITCAGAAACCAGATGCCCAGCCCTACCTCAACTGGAA 1413

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137 snMetThrProProLeuLeuHisHisaspLeuLysThrGlnasnIleLeu ::::::::		153	
154 LeuaspasnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTr 		170 664	
170 pargMetMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluG ::::		187 705 ·	
187 lyGlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLys :: ::		203 752	
204 SerArgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTr :::		220 802	
220 pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG		237 849	
237 InileMetTyrSerValSerGlnGlyHisArgProValileAsnGlu ::: ::: ::: :::		252 899	
253 GluSerLeuProTyrAspileProHisArgAlaArgMetil		266 943	
266 eSerLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerP::: ::::		283 993	
283 heLeuLysCysLeulleGluLeuGluProValLeuArgThrPheGluGlu ::: :::		299 1040	
300 IleThrPheLeuGlualaVallleGlnLeuLysLysThrLysLeuGlnSe ::: :::: :::::: 1041AACAATATGAATGCTGCTGTCTCCACGGTAAAGGATTTCCTGTCTCA		316 1087	
316 rValSerSer.AlaileHisLeuCysAspLysLysMetGlu .:::		330 1137	
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337 .Valasn.HisGlyProGlnGluGluSerCysGlySer ::		348 1237	
349 SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuPr 		365 1263	
365 oAlaProGlnAspAsnAspPheLeuSerArgLysAla		377 1313	
377		377	
1314 TGGACAGCAGGCACATCTTCAGATTCGATGGCCCAACCTCCCCAGACTCC		1363	
378 GlnAspCysTyrPheMetLysLeuHisHisCysPro		390	

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1490 AAATCCAGTAACAGGGCGACCGCTCGTTAACATATACAACTGCTCTGGGG 1539
                                      1414 CACCAAGTCCTGGACCCCGAGGGAATCAGGGGGCTGAGAG......1453
                                                                                                       GENERAL INFORMATION:
APPLICANT: ECKET, JOSEPH R.
APPLICANT: KIEDET, JOSEPH J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Macklewicz and
ADDRESSE: No. 5377065ris
STREET: One Liberty Place - 46th Floor
                                                                             407 ysAspHisLysThrThrProCysSerSerAlallelleAsnProLeuSer 423
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Gaps: 12
Percent Identity: 30.721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/928,464 FILING DATE: 19920810
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19920810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568 3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2890 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
    Sequence 1, Application US/07928464
    Patent No. 5367065
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US-09-445-223-1 x US-07-928-464-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compa
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1.861
63.323
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; LOCATION: 118..2583
US-07-928-464-1
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: lin
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Phil
STATE: PA
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2285
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                                                                                                                                                                                                                                                                                            1766 ATCTTAATATAAAAGAAAGATTGGAGCAGGTTCCTTTGGCACTGTCCAC 1815
                                                                                                                                                                                                                                                                                                                                                                             :::|||:::|||:::|||:::|
1816 CGTGCTGAGGTGGCTCGGATGTTGCTGTGAAATTCTCATGGAGCA 1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2201 TIGGICTCTCGCGATIGAAGGCCAGCACGTTTCTTTCTCTCGAAGTCAGCA 2250
                                                                                             1675 ATGAATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGCAAATAGGGA 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 heGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSer 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 ..ArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnPro 277
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                                                                                                                                                                                                                                              20 spleuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                      50 .HisIleHisThrProLeuLeuAspSerGluArg...LysAspValLeuA
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                                                                                                                                                 13 ......IleProTyrHisLysLeuAlaA
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                                              1 MetAsnGlyGluAlaIleCysSerAlaLeuProThr.......
to: 2890
Align seg 1/1 to: US-07-928-464-1 from: 1
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2494 TGGAAGCGTCCATCATTTGCAACTATAATGGACTTGCTAAGACCATTGAT 2543
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                                                                                                                                                                                                                  seq_documentation_block:
    Sequence 1, Application PC/TUS9307347
    GENERAL INFORMATION:
    APPLICANT: Ecker, Joseph R.
    TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                            seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US93-07347-1
278 AspGluArgProSerPheLeuLysCysLeuIleGluLeuGluProValLe 294
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ADDRESSEE: Norris
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Gaps: 12
Percent Identity: 30.721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/07347 CLASSIFICATION .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty Place - 46th Floor CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1
TELECOMMUTCATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2890 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
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US-09-445-223-1 x PCT-US93-07347-1
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1.861
63.323
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                                                                                                                              2544 CAAATCA 2550
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Percent Similarity:
                                                                                      294 uArgThr 296
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STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
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, LOCATION:
PCT-US93-07347-1
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seq_documentation_block:

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2286 GCGAGATGAGCCGTCTAATGAA......AAGTCAGATGTGT 2320
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2371 GGTAACTTA...AATCCGGCTCAGGTTGTAGCTGCGGTTGGTTTCAAGTG 2417
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                                                                                                                                                                                                                                             .........GCTGAGCGTGTTAATGAGTTCTTAA 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .. ArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnPro 277
                                              1766 ATCTTAATATAAAAGAAAGATTGGAGCAGGTTCCTTTGGCACTGTCCAC 1815
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1816 CGTGCTGAGTGGCATGTTCCTGTGAAATTCTCATGGAGCA 1865
                                                                                                                                                                                                                                                                                                                                                     1901 GAGAGGTTGCGATAATGAAACGCCTTCGCCACCCTAACATTGTTCTCTTC 1950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 sThrGlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 heGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSer 181
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20. spLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArg 36
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                                                                                                     37 HisAlaAspTrpArg...ValGlnValAlaValLySHisLeu.
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                                                                                                                                                                                                                                                       1866 AGACTTCCAT
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seq_name: /cgn1_7/ptodata/1/ina/5A_COMB.seq:US-08-003-311B-1

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1766 ATCTTAATATAAAAGAAAAGATTGGAGCAGGTTCCTTTGGCACTGTCCAC 1815
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13 .....IleProTyrH1sLysLeuAlaA 20
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Gaps: 12
Percent Identity: 30.721
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                                                                                                                                                                                                                                                                                                      January 12, 1993
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-003-311B-1
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US-09-445-223-1 x US-08-003-311B-1
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LOLA NUMBER: 34,299
REGISTRATION NUMBER: UP
REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: August 10, 1
                                                                                                                                                                                                                                                                                                WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                          Lori Y. Beardell
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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1.861
63.323
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STRANDEDNESS: single
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118..2583
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MOLECULE TYPE:
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                                                                                                                                                                                                   STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY:
, LOCATION:
US-08-003-311B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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APPLICANT: Ecker, Joseph R.

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                                                                      50 .HisIleHisThrProLeuLeuAspSerGluArg...LysAspValLeuA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 yrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe
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                                                                                                                                                                                                                                                                              LeuGlyIleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMe
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Sequence 1, Application US/08261432 Patent No. 5602322 GENERAL INFORMATION:

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1766 ATCTTAATATAAAGAAAGATTGGAGCAGGTTCCTTTGGCACTGTCCAC 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1725 ACTIGGACTIGAIGGIGAIGAIAIGGACAICCCGIGG......IGIG 1765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 spLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArg 36
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APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene TITLE OF INVENTION: and Mutations
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSE: No. 5603322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 .HisileHisThrProLeuLeuAspSerGluArg...LysAspValLeuA ::::|||| ::::::: |||||
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Gaps: 12
Percent Identity: 30.721
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                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLORPY GISK
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION BOOM
PRIOR APPLICATION BOOM
PRIOR APPLICATION WOMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LOIT Y: Beachell
RECISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: 34,293
TELECHONE: 215-568-3190
TELECHONE: 215-568-3190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-445-223-1 x US-08-261-432-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376.00
1.861
63.323
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                        CITY: Phil
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                       COUNTRY:
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2286 GCGAGATGAGCCGTCTAATGAA......AAGTCAGATGTGT 2320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||:::::|||||||:::
321 ACAGCTTCGGGGTCATCTTGTGGGAGCTTGCTACATTGCAACAACCATGG 2370
                                                                                                                                                                                                                   2201 TIGGICTCICGCGATIGAAGGCCAGCACGTITCTITCCICGAAGICAGCA 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .........GAGATCCCGCGTAATC 2443
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.......GCTGAGCGTGTTAATGAGTTCTTAA 1900
                                                                                                                        1901 GAGAGGTTGCGATAATGAAACGCCTTCGCCACCCTAACATTGTTCTCTTC 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2251 GCTGGAACCCCCGAG..........TGGATGGCACCAGAAGTCCT 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2444 TGAATCCTCAGGTTGCAGCCATAATCGAGGGTTGTTGGACCAATGAGCCA 2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSer 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yrserTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 GluAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGlyHi 246
                                                                                                                                                                                                                                                                                                         98 tProAsnGlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 ValAsnTyrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLy 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 sThrGlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 LysSerAlaProGluGlyGlyThrIleIleTyrMetProProGlu..... 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 sArgProVallleAsnGluGluSerLeuProTyrAspIleProHis.... 261
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APPLICANT: HSU, HAILING
APPLICANT: GOEDBEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2051 AATTAGATGAGACGTCGCCTGAGTATGGCTTATGATGTGGCTAAGGGA
                                                                                                                                                                                                                                                                                                                                           rgGluAlaGluIleLeuHisLysAlaArgPheSerTyrIlePheProIle
                                                                                                                                                                                    82 LeuGlyIleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMe
                                                                                                                                                                                                                                                                                                                                                                                                                              115 spValAlaTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 .AsnTyrGluProGlyGlnLysSerArgAlaSerIleLysHisAspIleT
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Patent No. 6211337
GENERAL INFORMATION:
APPLICANT: BAICHWAL, VIJAY R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block
   1866 AGACTTCCAT...
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TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AGAACCCAGGGACTCATGATCATGAAAACAGTGTACAAGGGGCCCAACT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 euAspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLys 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAGACACAGCCGGGTGGAAGCTCCTGGGCGTCATCATAGAGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 389
Gaps: 12
Percent Identity: 28.792
                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA:
FILLIG DATE: US/09/132,118
FILLIG DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-132-118-1 from: 1 to: 2016
                                                                                 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 IGCIGAAAGCCGAGAIGAGIACTCCG
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US-09-445-223-1 x US-09-132-118-1
                        ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2016 base pairs
                                                                                                                                                 USA

2.1P: 94010

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopov
COMFUTER: TEV
OPERATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.716
55.270
TITLE OF INVENTION: TUR
TITLE OF INVENTION: AS,
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                           CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Percent Similarity:
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STRANDEDNESS
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US-09-132-118-1
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4etTh 139 393	laspa 156 GATA 442	:9Met 172 :: GATG 492	186 GACGG 542	1 196 SCACC 592	leLys 209 627	Argly 226 :::1 Aataa 674	cVals 243 :::: CATAA 724	colyr 257 SAAGA 774	YTrpAl 274 CTGGGA 806	eGluLeuG 291 ::::::: AAAATTTA 856	alile 307 	LeuGl 315 :::{ ATGCA 956	sLeuc 324 : : Trcag 1006	isGly 340 rGGGT 1056	Glyse 357	pPheLeus 374 : cagccrgc 1123	
ArgileLeunisGluileAlaLeuGlyValAsnTyrLeunisAsnM :: AGGATAATTTTGGAAATCATTGAAGGAATGTGCTACTTACATGGA.	ProProLeuLeuhisHisAspLeuLysThrGlnAsnIleLeuLeuAspA ::::::	snGluPheHisValLysIlealaAspPheGlyLeuSerLysTrpArgMe 	MetSerLeuserGlnSerargserbysseralaProglu ::::: TGGAGCAAACTGAATGAAGAGCACAATGAGCTGAGGGAAGTGGAG			SASPILETYRSETTYRALAVALILETHFTPGLUVALLEUSErArgLy ::: :: GATGTGTACAGCTTTGCTGTAGTACTCTGGGGGATATTTGCAAATAA	SGInProPheGluAspValThrAsnProLeuGlnIleMetTyrSerValS ::: ::: ::: GAGCCATATGAAATGCTATCTGTGAGCAGCAGTTGATAATGTGCATAA	erGlnGlyHisArgProVallleAsnGluGluSerLeuProTy: ::::: :: ::::::: AATCTGGGAACAGGCAGATGTGGATGACACACTGAGTACTGCCCAAG	aArgMetIleSerLeulleGluSerGl ::::: arcaGrCrCarGaaGCrCTG	aGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGluLe 	lubrovalLeuArgThrPheGluGluIleThrPheLeuGluAlaValIle :	GInLeuLysLysThrLysLeuGl ::: AGTTTAAAGAAAGTATTCAAACGAAAATGCAGTTGTGAAGAGAATGCA	GTGTGGCAGTACCTTCAAGCGGTCAAATTCAG	ysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGly :: ::::: :::::: :::: CCACAGAACAGCCTGGTTCACTGCAGTTCCCAGGGACTTGGGATGGGT	ProGlnGluGluSerCysGlySerSerGlnLeuHisGluAsnSer(erLeuProAlaProGlnAspAsnAs CCACAAGAAGAATGAGCC	1
ArgileLeuHisGluile ::: AGGATAATTTTGGAAATC	rProProLeuLeuHisHi :::::: .AAAGGCGTGATACACA.	snGluPheHisValLys] ::: ATGACTTCCACATTAAGA	MetSerLeuSerGlnSer TGGAGCAAACTGAATAA	CACCGCTAAGAAGAATG	AsnTyr(TGAATGACGTCAACGCA	н.	sGlnProPheGluAspVa ::: ::: ::: GGAGCCATATGAAAATG	erGlnGlyHisArgPro) ::::: AATCTGGGAACAGGCCA(AsplleProHisArgAla ::: GAAATT	aGlnAsnProAspGluA) AGCGAATCCGGAAGCTC	luProValLeuArgThr :: GGCCTTTTTATTTAAGT		nSerVal	ysasplyslysmet :: :::::: CCaCaGaaCaGCCTGGT	ProGlnGluGluSerCy: 	rProGluThrSerArgS	erargiysaladinasp :: agagtaaactccaagac
123	139 394	156	173	187	197 593	210	226	243	258	274	291	308	315	324	341	357 1096	374

seq_name: /cgn1_7/ptodata/1/ina/5A_COMB.seq:US-08-444-005-16

158 GCATTGAGCACAACGAGGCCCTCTTGGAGGAGGAGAAGATGATGATGAACAGA 207 89 uPheLeuGly11eValThrGluTyrMetProAsnGlySerLeuAsnGluL 106 109 AGAACCCAGGGACTCATGATCATGAAACAGTGTACAAGGGGCCCCAACT 157 208 CIGAGACACACCGGGTGGTGAAGCTCCTGGGCGTCATCATAGAGGAAGG 257 24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr 40 40 pArgValGln...ValAlaValLySHisLeuHisIleHisThrProLeuL 56 56 euAspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLys 72 73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl 89 Length: 390 Gaps: 13 Percent Identity: 29.231 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005 Align seg 1/1 to: US-08-444-005-16 from: 1 to: 2137 STREET: 225 Franklin Street, Suite 3100 CITY: Boston STATE: WA COUNTRY: USA ZIP: 0210-0-2 APPLICANT: Leder, Philip
APPLICANT: Seed, Brian
APPLICANT: Stanger, Ben Z.
APPLICANT: Lee, Tae-Ho
APPLICANT: Lee, Tae-Ho
APPLICANT: Kim, Emily
TITLE OF INVENTION: CELL DEATH PROTEIN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: 00383/026001 Sequence 16, Application US/08444005 Patent No. 5674734 CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 0038
TELECHMONICATION INFORMATION:
TELEPHONE: 617/542-6770
TELEPHONE: 617/542-6906 TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGHH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single alignment_block: US-09-445-223-1 x US-08-444-005-16 369.00 1.732 54.615 ; MOLECULE TYPE: DNA US-08-444-005-16 seg_documentation_block: GENERAL INFORMATION: Quality: Ratio: Percent Similarity: FILING DATE: alignment_scores:

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GICTCTTCAACTTGATTGTGTGGCAGTACCTTCAAGCCGGTCAAATTCAG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1057 ccrerecadearccreerrrecrecrecarccadeac.......... 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 ysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGly 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 ProGlnGluGluSer...CysGlySerSerGlnLeuHisGluAsnSerGl 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 ySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATT.....ATCAGTCTCATGAAGCTCTGGGGA 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 aGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGluLeuG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               807 AGCGAATCCGGAAGCTCGGCCGACATTTCCTGGCATTGAAGAAAATTTA 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIle 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCTTTTTTATTTAAGTCAATTAGAAGAAAGTGTAGAAGAGGACGTGAAG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ThrLysLeuGl 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....SerSerAlaIleHisLeuC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 HisAspileTyrSerTyrAlaValIleThrTrpGluValLeuSerArgLy 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....GATGTATACAGCTTTGCTGTAGTACTCTGGGGGGATATTTGCAAATAA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerValS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          675 GGAGCCATATGAAATGCTATCTGTGAGCAGCAGTTGATAATGTGCATAA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erGlnGlyHisArgProValIleAsnGlu.....GluSerLeuProTyr 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::::|||:::|||||||| :::::::::
AATCTGGGAACAGGCCAGATGTGGATGACATCACTGAGTACTGCCCAAGA 774
                                                                                                                                                                                                                                             snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 172
                                                                                                                                                                                                                                                                                                                                                           187 .....GlyGlyThrIleIleTyrMetProProGlu... 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 MetSerLeuSerGlnSerArgSerSerLysSerAlaProGlu...... 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 GAAGTACTCCCTGGTGATGCAGTACATGGAGAGGGCAACCTGATGCACG 307
                                                                    euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
                                                                                                                                                      123 ArgileLeuHisGluileAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
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907 AGTTTAAAGAAAGAGTATTCAAACGAAAATGCAGTTGTGAAGAGAATGCA
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                                                                                                                                                                                  493 TGGAGCAAACTGAATAATGAAGAGCACAATGAGCTGAGGGAAGTGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLeuLysLys.....
                                                                                                              308 TGCTGAAAGCCGAGATGAGTACTCCG.
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Sequence 1, APPLICATION US/09161443A
Sequence 1, APPLICATION US/09161443A
BAPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF RIP-1 EXPRESSION
FILE REFERENCE: RTS-0011
CURRENT APPLICATION NUMBER: US/09/161,443A
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 CIGGACAGCGAGGCTTTGGGAAGGIGTCTCTGTGTTTCCAC..... 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LeuserArgGlyAlaSerGlyThrValSerSerAlaArgH1sAlaAspTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl
                                                                                                         seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-09-161-443-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 389
Gaps: 12
Percent Identity: 28.792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-161-443-1 from: 1
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                                                                    1121 TGCAGAGTAAACTCCAAGAC 1140
                                    373 euSerArgLysAlaGlnAsp 379
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Quality: 369.00
Ratio: 1.716
Ratio: 1.716
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(2016)
                                                                                                                                            seq_documentation_block
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OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2141
OTHER INFORMATION:
FEATURE:
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LOCATION: 2496
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374 erArgLysAlaGlnAsp 379

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1057 ccrgrggaggagrccrggrrrgcrccrrggaggagcac.....1095
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                                                                                                                                                                                                                                                                                                                                                                   GlnLeuLysLys.....ThrLysLeuGl 315
                                               euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
                                                                                            308 TGCTGAAAGCCGAGATGAGTACTCCG......CTTTCTGTAAAAGGA 348
                                                                                                                                            ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
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349 AGGATAATTTTGGAAATCATTGAAGGAATGTGCTACTTACATGGA..... 393
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258 GAAGTACTCCCTGGTGATGGAGTACATGGAGAAGGGCAACCTGATGCACG 307
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229 heGluAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGly 245
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                                            seq_name: /cgn1_7/ptodata/1/ina/5A_COMB.seq:US-08-700-575-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGATAT
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olda
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 210
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                                                                                                        Sequence 31, Application US/08700575
Patent No. 5817479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-700-575-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY 36749
REGISTRATION NUMBER: 36749
REFERENCE/DOCKET NUMBER: SP-1
TELECOMUNICATION INFORMATION:
TELECHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-445-223-1 x US-08-700-575-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
1124 AGAGTAAACTCCAAGAC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUENCH: 210 base pairs
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 367.00
Ratio: 5.319
Percent Similarity: 100.000
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                                                                                      seq_documentation_block
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                                                                                                                                                                                                                                                                                                                                                                                                           USA
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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sequence 1, Application US/08685625A
sequence 1, Application US/08685625A
Patent No. 5945301
GENERAL INFORMATION:
APPLICANT: WATSUMOTO, Kunihiro
APPLICANT: WATSUMOTO, Kunihiro
APPLICANT: MATSUMOTO, Kunihiro
APPLICANTON: TRANSDUCTION SYSTEM
STATE: Virginia
CONRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STATE: Virginia
CONPUTER: Virginia
STATE: Virginia
STATE: Virginia
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,625A
FILING DATE: 29-SEP-1995
ATTONEY MEDIUM INFORMATION:
BECT CHEASTIT INFORMATION:
BECT CHEASTIT INFORMATION:
BECT CHEASTIT INFORMATION:
BECT CHEASTIT INFORMATION:
BECT CHEASTICN MUMBER: US 6077
102 TTGAAGATGTCACCAATCCTTTGCAGATAATGTATAGTGTGTCACAAGGA 151
                                             13 IleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgClyAlaSe 29
                                                                                                                                                                                                                                             seq_name: /cgn1_7/ptodata/1/ina/5B_COMB.seq:US-08-685-625A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 589
Gaps: 29
Percent Identity: 25.127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-685-625A-1 from: 1 to: 2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weuth, Donna M.
REGISTRATION NUMBER: 36 607
REFERENCE/DOCKET NUMBER: 001560-267
TELECAMONICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-445-223-1 x US-08-685-625A-1
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315.50
1.119
47.878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 157..1893
US-08-685-625A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality: 3
Ratio: 1
Percent Similarity: 4
                                                                                                                                                                                          202 AGCACGT 208
                                                                                                                                         262 galaarg 264
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1094	attacagtatccttgtcactactctgatgaagggcagaggaactca	10
290		7
1044	31ubeu	N 60
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283	9 eGluSerGlyTrpAlaGlnAsnProAspGluArgProSer	26
944	GCCCATTGAG	6
269	uSerLeuProTyrAsplleProHisArgAlaArgMetileSerLeu	2
912	:::	œ
252	SlnileMetTyrSerValSerGlnGlyHisArgProValIl	7
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220	04. SerArgAlaSerIleLySHiSAspIleTyrSerTyrAlaValIleThrTr ::: 66. AGCAATTACAGTGAAAAGTGTGATGTCTTCAGCTGGGGTATTATCTCTG	9 6
765	:	7
203	yrMetProProGluAsnTyrGluProGlyGlnL	ä
726	GACCAATAATAAA	9
187	<pre>0 pargmetMetSerLeuSerGlnSerargSerSerLysSeralaPr</pre>	17
698	::: :::	. 64
170	AspAsnGluPheHisValLysIleAlaAspPheGlyLeuSe	Ä
154 648	39 hrproProfeuleuHisHisAspleuLysThrGlnAsnlleUeuLeu 	i is
598		S
139	eLeuHisGluIleAlaLeuGlyValAsn	Н
561		51
122	roAspValAl	Н
	7 TGGAATATGCAGAGGGGGCTCATTGTATAATGTGCTGCATGGTGCTGCT	4
95 466	78 ePheProIleLeuGlyIleCysAsnGluProGluPheLeuGlyIleValT	. 4
422	::: ::: TTTCATTGTGGAGCTCCGGCAGTTGTCGCGTCTGAACCATCCTA	'n
7.8	JArgGluAlaGluIleLeuHisLysAlaArgPheSerTyr	
61 372	ThrPr	i m
337		7
2 2	CONC. ACARGOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Ň

290		
1095	CACCAGCACAGGCTCGTTCATGGACATTGCTACAAATACCAGTAATA 1144	
291		
302	PheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerValSe 318 :: :: :: :: ::	
318	rSeralalleHisLeuCysAspLysLysMetGluLeuSerLeuAsnI 335 ::: ::: :::::: TGGACGCCTGAGCTTGGGAGCCTCTCGTGGAGCAGTGTGGAGAGCTTGC 1294	
335	leProValasnHisGlyProGlnGluGluGluSerCysGlySerSerGlnLeu 351 ::::::: ::::: :::: CCCCCACTTCCGAGGGCAAGAGGATGAGTGCTGAAATGTCTGAAATA 1341	
352	HisGluasnSerGlySerProGluThrSerAr 362 ::: :: :::	
362	gSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnA 379 ::: ATCCATCCAAGACTT	
379 1405	spCysTyrPheMetLysLeuH1sH1sCysProGlyAsnH1sSerTrpAsp 395	
396	SerThrileSerGlySerGln	
403		
412	ThrProcysSerSerAlallelleAsn	
422	uSerThralaGlyAsnSerGluArgLeuGlnPro	
434		
445	GluaspileValasnGlnMetThrGlualaCysLeuAsnGl 458 ::	
458		
475	luLeuValSerThrLysProThrArgThrSerLysVal	
488	ArgGlnLeuLeuAsp 492 ::::: AAAAGCTTTTAGAT 1803	

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